

SEQUENCE LISTING

<110> Flachmann, Ralf
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 Voeste, Dirk

<120> Use of astaxanthin-containing plants or parts of plants of the
 genus Tagetes as feedstuffs

<130> 13173-00004-US

<150> PCT/EP2003/009109
 <151> 2003-08-18

<150> DE 102 38 980.2
 <151> 2002-08-20

<150> DE 102 38 978.0
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<150> DE 102 38 979.9
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<150> DE 102 53 112.9
 <151> 2002-11-13

<150> DE 102 58 971.2
 <151> 2002-12-16

<160> 142

<170> PatentIn version 3.3

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<212> DNA

<213> Haematococcus pluvialis

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<221> CDS

<222> (166)..(1155)

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 Met Gln Leu Ala

gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag	225
Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys	
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Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp	
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gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg	321
Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro	
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Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile	
55 60 65	
aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac	417
Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His	
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Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp	
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Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser	
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Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr	
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Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met	
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Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	
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Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His	
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His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	
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aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg	801
Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
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Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala	
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 Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro
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cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg 993
 His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met
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 Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe
 280 285 290

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 Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg
 310 315 320

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 Gly Leu Val Pro Ala
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<212> PRT

<213> Haematococcus pluvialis

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 35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
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Leu Ser Gly Arg Gly Leu Val Pro Ala
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<222> (168)..(1130)

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ctccgtcttc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc 176
 Met His Val
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gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc 224
 Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
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agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc 272
 Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
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gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct 320
 Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
 40 45 50

cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc 368
 Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
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acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg 416

Thr	Trp	Thr	Ala	Val	Phe	Leu	His	Ala	Ile	Phe	Gln	Ile	Arg	Leu	Pro	
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Thr	Ser	Met	Asp	Gln	Leu	His	Trp	Leu	Pro	Val	Ser	Glu	Ala	Thr	Ala	
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cag	ctt	ttg	ggc	gga	agc	agc	agc	cta	ctg	cac	atc	gct	gca	gtc	ttc	512
Gln	Leu	Leu	Gly	Gly	Ser	Ser	Ser	Leu	Leu	His	Ile	Ala	Ala	Val	Phe	
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Ile	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Thr	His	Asp	
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Ala	Met	His	Gly	Thr	Ile	Ala	Leu	Arg	His	Arg	Gln	Leu	Asn	Asp	Leu	
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Leu	His	Arg	Lys	His	Trp	Glu	His	His	Asn	His	Thr	Gly	Glu	Val	Gly	
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Lys	Asp	Pro	Asp	Phe	His	Lys	Gly	Asn	Pro	Gly	Leu	Val	Pro	Trp	Phe	
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Ala	Ser	Phe	Met	Ser	Ser	Tyr	Met	Ser	Leu	Trp	Gln	Phe	Ala	Arg	Leu	
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Ala	Trp	Trp	Ala	Val	Val	Met	Gln	Met	Leu	Gly	Ala	Pro	Met	Ala	Asn	
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ctc	cta	gtc	ttc	atg	gct	gca	gcc	cca	atc	ttg	tca	gca	ttc	cgc	ctc	896
Leu	Leu	Val	Phe	Met	Ala	Ala	Ala	Pro	Ile	Leu	Ser	Ala	Phe	Arg	Leu	
		230					235					240				
ttc	tac	ttc	ggc	act	tac	ctg	cca	cac	aag	cct	gag	cca	ggc	cct	gca	944
Phe	Tyr	Phe	Gly	Thr	Tyr	Leu	Pro	His	Lys	Pro	Glu	Pro	Gly	Pro	Ala	
	245					250					255					
gca	ggc	tct	cag	gtg	atg	gcc	tgg	ttc	agg	gcc	aag	aca	agt	gag	gca	992
Ala	Gly	Ser	Gln	Val	Met	Ala	Trp	Phe	Arg	Ala	Lys	Thr	Ser	Glu	Ala	
260					265				270						275	
tct	gat	gtg	atg	agt	ttc	ctg	aca	tgc	tac	cac	ttt	gac	ctg	cac	tgg	1040
Ser	Asp	Val	Met	Ser	Phe	Leu	Thr	Cys	Tyr	His	Phe	Asp	Leu	His	Trp	
				280					285					290		
gag	cac	cac	agg	tgg	ccc	ttt	gcc	ccc	tgg	tgg	cag	ctg	ccc	cac	tgc	1088
Glu	His	His	Arg	Trp	Pro	Phe	Ala	Pro	Trp	Trp	Gln	Leu	Pro	His	Cys	
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cgc	cgc	ctg	tcc	ggg	cgt	ggc	ctg	gtg	cct	gcc	ttg	gca	tga			1130

Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
 310 315 320

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<212> PRT

<213> Haematococcus pluvialis

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Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala
 35 40 45

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
 50 55 60

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
 65 70 75 80

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
 85 90 95

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
 100 105 110

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
115 120 125

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
130 135 140

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
145 150 155 160

Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
165 170 175

Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
180 185 190

Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe
195 200 205

Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro
210 215 220

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala
225 230 235 240

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
245 250 255

Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
260 265 270

Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
275 280 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
290 295 300

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<212> DNA

<213> Agrobacterium aurantiacum

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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	
20 25 30	
gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
Ala Leu Trp Phe Leu Asp Ala Ala His Pro Ile Leu Ala Ile Ala	
35 40 45	
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	
cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	
gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
145 150 155 160	
gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
180 185 190	
gac cgc cac aat gcg ccg tcg tcg ccg atc agc gac ccc gtg tcg ctg	624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	
195 200 205	
ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac	672

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
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 Thr Ala

<210> 6

<211> 242

<212> PRT

<213> Agrobacterium aurantiacum

<400> 6

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 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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Thr Ala

<210> 7

<211> 1631

<212> DNA

<213> Alcaligenes sp.

<220>

<221> CDS

<222> (99)..(827)

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 Met Ser Gly Arg Lys Pro
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ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164
 Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile
 10 15 20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212
 Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp
 25 30 35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260
 Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr
 40 45 50

tgg ctg tgc gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg 308

Trp	Leu	Ser	Val	Gly	Leu	Phe	Ile	Ile	Ala	His	Asp	Ala	Met	His	Gly		
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Ser	Val	Val	Pro	Gly	Arg	Pro	Arg	Ala	Asn	Ala	Ala	Ile	Gly	Gln	Leu		
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gcg	ctg	tgg	ctc	tat	gcg	ggg	ttc	tgc	tgg	ccc	aag	ctg	atc	gcc	aag		404
Ala	Leu	Trp	Leu	Tyr	Ala	Gly	Phe	Ser	Trp	Pro	Lys	Leu	Ile	Ala	Lys		
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cac	atg	acg	cat	cac	cgg	cac	gcc	ggc	acc	gac	aac	gat	ccc	gat	ttc		452
His	Met	Thr	His	His	Arg	His	Ala	Gly	Thr	Asp	Asn	Asp	Pro	Asp	Phe		
ggt	cac	gga	ggg	ccc	gtg	cgc	tgg	tac	ggc	agc	ttc	gtc	tcc	acc	tat		500
Gly	His	Gly	Gly	Pro	Val	Arg	Trp	Tyr	Gly	Ser	Phe	Val	Ser	Thr	Tyr		
ttc	ggc	tgg	cga	gag	gga	ctg	ctg	cta	ccg	gtg	atc	gtc	acc	acc	tat		548
Phe	Gly	Trp	Arg	Glu	Gly	Leu	Leu	Leu	Pro	Val	Ile	Val	Thr	Thr	Tyr		
gcg	ctg	atc	ctg	ggc	gat	cgc	tgg	atg	tat	gtc	atc	ttc	tgg	ccg	gtc		596
Ala	Leu	Ile	Leu	Gly	Asp	Arg	Trp	Met	Tyr	Val	Ile	Phe	Trp	Pro	Val		
ccg	gcc	gtt	ctg	gcg	tgc	atc	cag	att	ttc	gtc	ttc	gga	act	tgg	ctg		644
Pro	Ala	Val	Leu	Ala	Ser	Ile	Gln	Ile	Phe	Val	Phe	Gly	Thr	Trp	Leu		
ccc	cac	cgc	ccg	gga	cat	gac	gat	ttt	ccc	gac	cgg	cac	aac	gcg	agg		692
Pro	His	Arg	Pro	Gly	His	Asp	Asp	Phe	Pro	Asp	Arg	His	Asn	Ala	Arg		
tgc	acc	ggc	atc	ggc	gac	ccg	ttg	tca	cta	ctg	acc	tgc	ttc	cat	ttc		740
Ser	Thr	Gly	Ile	Gly	Asp	Pro	Leu	Ser	Leu	Leu	Thr	Cys	Phe	His	Phe		
ggc	ggc	tat	cac	cac	gaa	cat	cac	ctg	cat	ccg	cat	gtg	ccg	tgg	tgg		788
Gly	Gly	Tyr	His	His	Glu	His	His	Leu	His	Pro	His	Val	Pro	Trp	Trp		
cgc	ctg	cct	cgt	aca	cgc	aag	acc	gga	ggc	cgc	gca	tga	cgcaattcct				837
Arg	Leu	Pro	Arg	Thr	Arg	Lys	Thr	Gly	Gly	Arg	Ala						
cattgtcgtg	gcgacagtcc	tcgtgatgga	gctgaccgcc	tattccgtcc	accgctggat												897
tatgcacggc	cccctaggct	ggggctggca	caagtcccat	cacgaagagc	acgaccacgc												957
gttggaagaag	aacgacctct	acggcgctcgt	cttcgcgggtg	ctggcgacga	tcctcttcac												1017
cgtgggcgcc	tattggtggc	cgggtgctgtg	gtggatcgcc	ctgggcatga	cggtctatgg												1077
gttgatctat	ttcatcctgc	acg															

gcaggatctg aagcggtcgg gtgtcctgcg cccccaggac gagcgccgt cgtgatctct 1317
 gatcccgcg tggccgcatg aaatccgacg tgctgctggc aggggccggc cttgccaacg 1377
 gactgatcgc gctggcgatc cgcaaggcgc ggccccgacct tcgcgtgctg ctgctggacc 1437
 gtgcggcggg cgccctcggac gggcatactt ggtcctgcca cgacaccgat ttggcgccgc 1497
 actggctgga ccgcctgaag ccgatcaggc gtggcgactg gcccgatcag gaggtgcggt 1557
 tcccagacca ttgcgaagg ctccggggccg gatatggctc gatcgacggg cgggggctga 1617
 tgcgtgcggt gacc 1631

<210> 8

<211> 242

<212> PRT

<213> *Alcaligenes* sp.

<400> 8

Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu
 1 5 10 15

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
 20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
 35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
 100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
 115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
225 230 235 240

Arg Ala

<210> 9

<211> 729

<212> DNA

<213> *Paracoccus marcusii*

<220>

<221> CDS

<400> 9

atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc aca agc ctg 48
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
20 25 30

gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144
Ala Leu Trp Phe Leu Asp Ala Ala His Pro Ile Leu Ala Val Ala
35 40 45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn 65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp 85 90 95	288
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr 100 105 110	336
gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala 115 120 125	384
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro 130 135 140	432
gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr 145 150 155 160	480
gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe 165 170 175	528
gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro 180 185 190	576
gac cgc cat aat gcg ccg tcg tcg ccg atc agc gac cct gtg tcg ctg Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu 195 200 205	624
ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His 210 215 220	672
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp 225 230 235 240	720
acc gca tga Thr Ala	729

<210> 10

<211> 242

<212> PRT

<213> Paracoccus marcusii

<400> 10

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu 1 5 10 15
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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

Thr Ala

<210> 11

<211> 1629

<212> DNA

<213> *Synechococcus* sp.

<220>

<221> CDS

<400> 11

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Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu	
1 5 10 15	
gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta	96
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu	
20 25 30	
gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg	144
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met	
35 40 45	
ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac	192
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His	
50 55 60	
gaa ttt atc ttt ctg ggg cgg gtg ttg cag gag cta aat tta gcc cag	240
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln	
65 70 75 80	
tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg	288
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly	
85 90 95	
ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt	336
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys	
100 105 110	
gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa	384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln	
115 120 125	
ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt	432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe	
130 135 140	
aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg	480
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp	
145 150 155 160	
gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg	528
Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala	
165 170 175	
ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat	576
Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn	

180	185	190	
gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys 195 200 205			624
tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met 210 215 220			672
atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly 225 230 235 240			720
ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln 245 250 255			768
ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu 260 265 270			816
aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg 275 280 285			864
gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu 290 295 300			912
caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly 305 310 315 320			960
gaa cga ctg gaa cgg cgc act gtg aac aat aac gaa gcc att tta aaa Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys 325 330 335			1008
atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly 340 345 350			1056
ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His 355 360 365			1104
gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala 370 375 380			1152
aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met 385 390 395 400			1200
gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr 405 410 415			1248
cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr			1296

420	425	430	
gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg			1344
Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr			
435	440	445	
gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa			1392
Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu			
450	455	460	
agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc			1440
Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val			
465	470	475	480
tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta			1488
Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu			
485	490	495	
ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca			1536
Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr			
500	505	510	
ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga			1584
Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg			
515	520	525	
aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa			1629
Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp			
530	535	540	
<210>	12		
<211>	542		
<212>	PRT		
<213>	Synechococcus sp.		
<400>	12		
Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu			
1	5	10	15
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu			
20	25	30	
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met			
35	40	45	
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His			
50	55	60	
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln			
65	70	75	80

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
85 90 95

Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
130 135 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
145 150 155 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
165 170 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
210 215 220

Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
225 230 235 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
245 250 255

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
 325 330 335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
 340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
 355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
 370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
 385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
 405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
 420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
 435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
 450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
 465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
 485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
 500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
 515 520 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
 530 535 540

<210> 13

<211> 776

<212> DNA

<213> Bradyrhizobium sp.

<220>

<221> CDS

<222> (1)..(774)

<400> 13

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Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg	
1 5 10 15	
gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc	96
Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile	
20 25 30	
atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg	144
Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro	
35 40 45	
ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag	192
Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln	
50 55 60	
acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac	240
Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His	
65 70 75 80	
ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag	288
Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln	
85 90 95	
ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc	336
Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val	
100 105 110	
gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat	384
Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp	
115 120 125	
ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt	432
Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe	
130 135 140	
ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc	480
Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val	
145 150 155 160	
tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg	528
Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu	
165 170 175	
ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc	576
Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr	
180 185 190	

ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat 624
 Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg 672
 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat 720
 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg 768
 Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

cgt gac ta 776
 Arg Asp

<210> 14

<211> 258

<212> PRT

<213> Bradyrhizobium sp.

<400> 14

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
 1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
 50 55 60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp

115

120

125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

Arg Asp

<210> 15

<211> 777

<212> DNA

<213> Nostoc sp.

<220>

<221> CDS

<400> 15

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 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu 35 40 45	144
ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala 50 55 60	192
atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His 65 70 75 80	240
gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn 85 90 95	288
ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys 100 105 110	336
gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp 115 120 125	384
tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp 130 135 140	432
tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly 145 150 155 160	480
tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu 165 170 175	528
aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val 180 185 190	576
caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly 195 200 205	624
ggg tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe 210 215 220	672
tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His 225 230 235 240	720
gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile 245 250 255	768
tct tta taa Ser Leu	777

<210> 16

<211> 258

<212> PRT

<213> Nostoc sp.

<400> 16

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
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 20 25 30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
 225 230 235 240

Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

Ser Leu

<210> 17

<211> 1608

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (3)..(971)

<400> 17

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 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
 1 5 10 15

ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 20 25 30

tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143
 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
 35 40 45

cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191
 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
 50 55 60

tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga 239
 Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly
 65 70 75

acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca 287
 Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala
 80 85 90 95

ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa 335
 Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys
 100 105 110

cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc	383
Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly	
115 120 125	
gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac	431
Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His	
130 135 140	
atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc	479
Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu	
145 150 155	
ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat	527
Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr	
160 165 170 175	
gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac	575
Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His	
180 185 190	
aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg	623
Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu	
195 200 205	
ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc	671
Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly	
210 215 220	
ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg	719
Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu	
225 230 235	
ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg	767
Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu	
240 245 250 255	
gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg	815
Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met	
260 265 270	
aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt	863
Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly	
275 280 285	
ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att	911
Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile	
290 295 300	
cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg	959
Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp	
305 310 315	
tcc aag cgg tag ggtgcggaac caggcagcgt ggtttcacac ctcatgcctg	1011
Ser Lys Arg	
320	
tgataagggtg tggctagagc gatgcgtgtg agacgggtat gtcacgggtcg actggtctga	1071
tgccaatgg catcgcccat gtctggtcat cacgggctgg ttgcctgggt gaaggatgat	1131

cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc 1191
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 ggctcgtgcc agaaatggg agtgatgac tgtgacgctg tacattgcag gcaggtgaga 1551
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<210> 18

<211> 322

<212> PRT

<213> Haematococcus pluvialis

<400> 18

Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile Gly
 1 5 10 15

Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser
 20 25 30

Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg
 35 40 45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
 50 55 60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
 65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
 85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
 100 105 110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
 115 120 125

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met

130

135

140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
 145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
 165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
 180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
 195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
 210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
 225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
 245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
 260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
 275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
 290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
 305 310 315 320

Lys Arg

<210> 19

<211> 1503

<212> DNA

<213> Tomato

<220>

<221> CDS

<400> 19

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1 5 10 15	
cat cat ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat	96
His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His	
20 25 30	
cat aat ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt	144
His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val	
35 40 45	
tgt gtt aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc	192
Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr	
50 55 60	
aaa aag gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa	240
Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys	
65 70 75 80	
ggg gtt gtt gtg gat ctt gct gtg gtt ggt ggt ggc cct gca gga ctt	288
Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu	
85 90 95	
gct gtt gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att	336
Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile	
100 105 110	
gat ccg aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg	384
Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val	
115 120 125	
gat gaa ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg	432
Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp	
130 135 140	
tct ggt gca gca gtg tac att gat gat aat acg gct aaa gat ctt cat	480
Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His	
145 150 155 160	
aga cct tat gga agg gtt aac cgg aaa cag ctg aaa tcg aaa atg atg	528
Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met	
165 170 175	
cag aaa tgt ata atg aat ggt gtt aaa ttc cac caa gcc aaa gtt ata	576
Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile	
180 185 190	
aag gtg att cat gag gaa tcg aaa tcc atg ttg ata tgc aat gat ggt	624
Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly	
195 200 205	
att act att cag gca acg gtg gtg ctc gat gca act ggc ttc tct aga	672
Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg	
210 215 220	

tct ctt gtt cag tat gat aag cct tat aac ccc ggg tat caa gtt gct Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala 225 230 235 240	720
tat ggc att ttg gct gaa gtg gaa gag cac ccc ttt gat gta aac aag Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys 245 250 255	768
atg gtt ttc atg gat tgg cga gat tct cat ttg aag aac aat act gat Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp 260 265 270	816
ctc aag gag aga aat agt aga ata cca act ttt ctt tat gca atg cca Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro 275 280 285	864
ttt tca tcc aac agg ata ttt ctt gaa gaa aca tca ctc gta gct cgt Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg 290 295 300	912
cct ggc ttg cgt ata gat gat att caa gaa cga atg gtg gct cgt tta Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu 305 310 315 320	960
aac cat ttg ggg ata aaa gtg aag agc att gaa gaa gat gaa cat tgt Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys 325 330 335	1008
cta ata cca atg ggt ggt cca ctt cca gta tta cct cag aga gtc gtt Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val 340 345 350	1056
gga atc ggt ggt aca gct ggc atg gtt cat cca tcc acc ggt tat atg Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met 355 360 365	1104
gtg gca agg aca cta gct gcg gct cct gtt gtt gcc aat gcc ata att Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile 370 375 380	1152
caa tac ctc ggt tct gaa aga agt cat tcg ggt aat gaa tta tcc aca Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr 385 390 395 400	1200
gct gtt tgg aaa gat ttg tgg cct ata gag agg aga cgt caa aga gag Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu 405 410 415	1248
ttc ttc tgc ttc ggt atg gat att ctt ctg aag ctt gat tta cct gct Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala 420 425 430	1296
aca aga agg ttc ttt gat gca ttc ttt gac tta gaa cct cgt tat tgg Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp 435 440 445	1344
cat ggc ttc tta tcg tct cga ttg ttt cta cct gaa ctc ata gtt ttt His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe 450 455 460	1392

ggg ctg tct cta ttc tct cat gct tca aat act tct aga ttt gag ata 1440
 Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
 465 470 475 480

atg aca aag gga act gtt cca tta gta aat atg atc aac aat ttg tta 1488
 Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu
 485 490 495

cag gat aaa gaa tga 1503
 Gln Asp Lys Glu
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<210> 20

<211> 500

<212> PRT

<213> Tomato

<400> 20

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His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His
 20 25 30

His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
 35 40 45

Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 50 55 60

Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65 70 75 80

Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
 85 90 95

Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile
 100 105 110

Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
 115 120 125

Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp
 130 135 140

Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His

145		150		155		160									
Arg	Pro	Tyr	Gly	Arg	Val	Asn	Arg	Lys	Gln	Leu	Lys	Ser	Lys	Met	Met
			165						170					175	
Gln	Lys	Cys	Ile	Met	Asn	Gly	Val	Lys	Phe	His	Gln	Ala	Lys	Val	Ile
			180					185					190		
Lys	Val	Ile	His	Glu	Glu	Ser	Lys	Ser	Met	Leu	Ile	Cys	Asn	Asp	Gly
		195					200					205			
Ile	Thr	Ile	Gln	Ala	Thr	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg
	210					215					220				
Ser	Leu	Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala
225					230					235					240
Tyr	Gly	Ile	Leu	Ala	Glu	Val	Glu	Glu	His	Pro	Phe	Asp	Val	Asn	Lys
			245						250					255	
Met	Val	Phe	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Lys	Asn	Asn	Thr	Asp
			260					265					270		
Leu	Lys	Glu	Arg	Asn	Ser	Arg	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro
		275					280					285			
Phe	Ser	Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg
	290					295					300				
Pro	Gly	Leu	Arg	Ile	Asp	Asp	Ile	Gln	Glu	Arg	Met	Val	Ala	Arg	Leu
305					310					315					320
Asn	His	Leu	Gly	Ile	Lys	Val	Lys	Ser	Ile	Glu	Glu	Asp	Glu	His	Cys
			325						330					335	
Leu	Ile	Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val
			340				345					350			
Gly	Ile	Gly	Gly	Thr	Ala	Gly	Met	Val	His	Pro	Ser	Thr	Gly	Tyr	Met
		355					360					365			
Val	Ala	Arg	Thr	Leu	Ala	Ala	Ala	Pro	Val	Val	Ala	Asn	Ala	Ile	Ile
	370					375					380				
Gln	Tyr	Leu	Gly	Ser	Glu	Arg	Ser	His	Ser	Gly	Asn	Glu	Leu	Ser	Thr

385 390 395 400

Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
 405 410 415

Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
 420 425 430

Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
 435 440 445

His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
 450 455 460

Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
 465 470 475 480

Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu
 485 490 495

Gln Asp Lys Glu
 500

<210> 21

<211> 195

<212> DNA

<213> Potato

<220>

<221> Intron

<400> 21

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atataatatt tcaaataattt ttttcaaaat aaaagaatgt agtatatagc aattgctttt 120

ctgtagttta taagtgtgta tatttttaatt tataactttt ctaatatatg accaaaattt 180

gttgatgtgc agctg 195

<210> 22

<211> 1155

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (6)..(995)

<400> 22

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    1             5             10             15

gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac      98
Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp
          20             25             30

gtg ttg cgt aca tgg gcg acc cag tac tgc ctt ccg tca gag gag tca      146
Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser
          35             40             45

gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc      194
Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser
          50             55             60

gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gcc      242
Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala
          65             70             75

gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg      290
Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu
          80             85             90             95

gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt      338
Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val
          100            105            110

agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg      386
Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu
          115            120            125

gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat      434
Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His
          130            135            140

ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga      482
Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg
          145            150            155

gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc      530
Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg
          160            165            170            175

aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct      578
Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro
          180            185            190

gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc      626
Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe
          195            200            205

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atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg 674
 Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp
 210 215 220

acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg 722
 Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val
 225 230 235

ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt 770
 Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe
 240 245 250 255

ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct 818
 Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser
 260 265 270

tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc 866
 Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser
 275 280 285

gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag 914
 Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu
 290 295 300

cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc 962
 His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg
 305 310 315

cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc 1015
 Arg Leu Ser Gly Arg Gly Leu Val Pro Ala
 320 325

cctgctgcca gctgggcatg caggttgtgg caggactggg tgaggtgaaa agctgcaggc 1075

gctgctgccc gacacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg 1135

tttgtagctg tcgagcttgc 1155

<210> 23

<211> 329

<212> PRT

<213> Haematococcus pluvialis

<400> 23

Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
 1 5 10 15

Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
 325

<210> 24

<211> 1111

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (4) .. (951)

<400> 24

tgc atg cta gag gca ctc aag gag aag gag aag gag gtt gca ggc agc 48
 Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser
 1 5 10 15

tct gac gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gaa 96
 Ser Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu
 20 25 30

gag tca gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca 144
 Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro
 35 40 45

cct tcc gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc 192
 Pro Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser
 50 55 60

tgg gcc gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc 240
 Trp Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr
 65 70 75

tcc ttg gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag 288
 Ser Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln
 80 85 90 95

ctg gtt agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt 336
 Leu Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe
 100 105 110

gtc ctg gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct 384
 Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala

115	120	125	
atg cat ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg			432
Met His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu			
130	135	140	
ggc aga gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg			480
Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu			
145	150	155	
cac cgc aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag			528
His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys			
160	165	170	175
gac cct gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc			576
Asp Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala			
180	185	190	
agc ttc atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca			624
Ser Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala			
195	200	205	
tgg tgg acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg			672
Trp Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu			
210	215	220	
ctg gtg ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc			720
Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe			
225	230	235	
tac ttt ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca			768
Tyr Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser			
240	245	250	255
ggc tct tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag			816
Gly Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln			
260	265	270	
gcg tcc gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac			864
Ala Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His			
275	280	285	
tgg gag cac cac cgc tgg ccc ttc gcc ccc tgg tgg gag ctg ccc aac			912
Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn			
290	295	300	
tgc cgc cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac			961
Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala			
305	310	315	
tgcagtgggc cctgctgccca gctgggcatg caggttgtgg caggactggg tgaggtgaaa			1021
agctgcaggc gctgctgccg gacacgttgc atgggctacc ctgtgtagct gccgccacta			1081
ggggagggggg tttgtagctg tcgagcttgc			1111

<210> 25

<211> 315

<212> PRT

<213> Haematococcus pluvialis

<400> 25

Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser
1 5 10 15

Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu
20 25 30

Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro
35 40 45

Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp
50 55 60

Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser
65 70 75 80

Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu
85 90 95

Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val
100 105 110

Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met
115 120 125

His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly
130 135 140

Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His
145 150 155 160

Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp
165 170 175

Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser
180 185 190

Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp
195 200 205

Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu

210

215

220

Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr
 225 230 235 240

Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly
 245 250 255

Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala
 260 265 270

Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp
 275 280 285

Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys
 290 295 300

Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala
 305 310 315

<210> 26

<211> 1031

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (6)..(1031)

<400> 26

gaagc atg cag cta gca gcg aca gta atg ttg gag cag ctt acc gga agc 50
 Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser
 1 5 10 15

gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac 98
 Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp
 20 25 30

gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gag gag tca 146
 Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser
 35 40 45

gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc 194
 Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser
 50 55 60

gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gct 242
 Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala

65	70	75	
gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg			290
Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu			
80	85	90	95
gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt			338
Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val			
	100	105	110
agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg			386
Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu			
	115	120	125
gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat			434
Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His			
	130	135	140
ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga			482
Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg			
	145	150	155
gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc			530
Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg			
160	165	170	175
aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct			578
Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro			
	180	185	190
gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc			626
Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe			
	195	200	205
atg tcc agc tac atg tgc atg tgg cag ttt gcg cgc ctc gca tgg tgg			674
Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp			
	210	215	220
acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg			722
Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val			
	225	230	235
ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt			770
Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe			
240	245	250	255
ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct			818
Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser			
	260	265	270
tca cca gcc gtc atg aac tgg tgg aag tgc cgc act agc cag gcg tcc			866
Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser			
	275	280	285
gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag			914
Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu			
	290	295	300
cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc			962
His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg			

305 310 315
 cgc ctg tct ggc cga ggt ctg gtt cct gcc gag caa aaa ctc atc tca 1010
 Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser
 320 325 330 335

 gaa gag gat ctg aat agc tag 1031
 Glu Glu Asp Leu Asn Ser
 340

 <210> 27

 <211> 341

 <212> PRT

 <213> Haematococcus pluvialis

 <400> 27

 Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
 1 5 10 15

 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

 Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

 Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

 Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser Glu
 325 330 335

Glu Asp Leu Asn Ser
 340

<210> 28

<211> 777

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> promoter

<400> 28
gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt 60
tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactggtcga 120
agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagtttagga 180
ccaaacatta tctacaaaca aagacttttc tctaacttg tgattccttc ttaaacccta 240
ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300
atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360
tatatatctc tttctttctta tttcccaaata taacagacaa aagtagaata ttggctttta 420
acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
tcacttagtt ttcatcaact tctgaactta cttttcatgg attaggcaat actttccatt 660
tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720
tctttcttct cattatatct cttgtcctct ccaccaaatc tcttcaacaa aaagctt 777

<210> 29

<211> 22

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 29
gcaagctcga cagctacaaa cc 22

<210> 30

<211> 24

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 30
gaagcatgca gctagcagcg acag

24

<210> 31

<211> 30

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 31
tgcattgctag aggcactcaa ggagaaggag

30

<210> 32

<211> 59

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 32
ctagctattc agatcctctt ctgagatgag tttttgctcg gcaggaacca gacctcggc

59

<210> 33

<211> 28

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 33
gagctcactc actgatttcc attgcttg

28

<210> 34

<211> 37.
 <212> DNA
 <213> Unknown
 <220>
 <221> primer_bind
 <223> Synthetic sequence
 <400> 34
 cgccggttaag tcgatgtccg ttgatttaaa cagtgtc 37

 <210> 35
 <211> 34
 <212> DNA
 <213> Unknown
 <220>
 <221> primer_bind
 <223> Synthetic sequence
 <400> 35
 atcaacggac atcgacttaa cggcgtttgt aaac 34

 <210> 36
 <211> 25
 <212> DNA
 <213> Unknown
 <220>
 <221> primer_bind
 <223> Synthetic sequence
 <400> 36
 taagcttttt gttgaagaga tttgg 25

 <210> 37
 <211> 212
 <212> DNA
 <213> Unknown

<220>

<221> Intron

<223> Synthetic sequence

<400> 37

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gtcgactacg taagtttctg cttctacctt tgatatatat ataataatta tcattaatta      60
gtagtaatat aatattttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt      120
gcttttctgt agttttataag tgtgtatatt ttaatttata acttttctaa tatatgacca      180
aaatttggtg atgtgcaggt atcaccggat cc                                     212

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<210> 38

<211> 1830

<212> DNA

<213> Tagetes erecta

<220>

<221> CDS

<222> (141)..(1691)

<400> 38

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ggcacgaggc aaagcaaagg ttgtttggtg ttgttggtga gagacactcc aatccaaaca      60
gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa      120
agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca      173
                Met Ser Met Arg Ala Gly His Met Thr Ala Thr
                1             5             10
atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg      221
Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
                15             20             25
aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa      269
Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln
                30             35             40
gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg      317
Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu
                45             50             55
ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc      365
Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser
60             65             70             75
cta tcc caa aag ctg cca agg gta cca ata gga gga gga gga gac agt      413
Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser
                80             85             90

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aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt	461
Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu	
95 100 105	
gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc	509
Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile	
110 115 120	
ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa	557
Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu	
125 130 135	
ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat	605
Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp	
140 145 150 155	
act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc	653
Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala	
160 165 170	
tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg	701
Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg	
175 180 185	
tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att	749
Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile	
190 195 200	
act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797
Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
205 210 215	
aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga	845
Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly	
220 225 230 235	
aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893
Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	
240 245 250	
gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941
Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
255 260 265	
cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
270 275 280	
tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
285 290 295	
cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085
Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
300 305 310 315	
atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act	1133
Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr	
320 325 330	

atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att	1181
Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile	
335 340 345	
cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt	1229
Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe	
350 355 360	
ggg gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta	1277
Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val	
365 370 375	
aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att	1325
Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile	
380 385 390 395	
tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca	1373
Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr	
400 405 410	
acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg	1421
Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg	
415 420 425	
aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag	1469
Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln	
430 435 440	
atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg	1517
Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu	
445 450 455	
ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act	1565
Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr	
460 465 470 475	
gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc	1613
Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser	
480 485 490	
ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga	1661
Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly	
495 500 505	
aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag	1711
Thr Met Leu Lys Ala Tyr Leu Thr Ile	
510 515	
tttagattat aggcacatct tgcatatata tatgtataaa ccttatgtgt gctgtatcct	1771
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<210> 39

<211> 516

<212> PRT

<213> Tagetes erecta

<400> 39

Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr
1 5 10 15

Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
20 25 30

Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
35 40 45

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
50 55 60

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
65 70 75 80

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
100 105 110

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
115 120 125

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
130 135 140

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
145 150 155 160

Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
165 170 175

Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
180 185 190

Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
195 200 205

Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
210 215 220

Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
 225 230 235 240

Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
 245 250 255

Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
 260 265 270

Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
 275 280 285

Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
 290 295 300

Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
 305 310 315 320

Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile
 325 330 335

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
 340 345 350

Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
 355 360 365

Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
 370 375 380

Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn
 385 390 395 400

Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
 405 410 415

Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430

Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445

Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460

Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
 485 490 495

Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala
 500 505 510

Tyr Leu Thr Ile
 515

<210> 40

<211> 445

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(445)

<223> Sense Fragment

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 aaacagatac aaggcgtgac tggatatttc tctctcgttc ctaacaacag caacgaagaa 120
 gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180
 ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagt 240
 caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300
 gaaagccggt ggatcggagc tgctttttgt tcaaatagaa cagaataagt ccatggatgc 360
 acagtctagc ctatcccaaa agtcccaag ggtaccaata ggaggaggag gagacagtaa 420
 ctgtatactg gatttggttg tcgac 445

<210> 41

<211> 446

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<223> Antisense Fragment

<400> 41

gaattcgcac gaggcaaagc aaagggtgtt tgttggtgtt gttgagagac actccaatcc	60
aaacagatac aaggcgtgac tggatatttc tctctcgttc ctaacaacag caacgaagaa	120
gaaaaagaat cattaactaac aatcaatgag tatgagagct ggacacatga cggcaacaat	180
ggcggtttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg	240
caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt	300
gaaagccggt ggatcggagc tgctttttgt tcaaatgcaa cagaataagt ccatggatgc	360
acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa	420
ctgtatactg gatttggttg gatcct	446

<210> 42

<211> 393

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<223> Sense Fragment

<400> 42

aagctttgga ttagcactga ttgtccagat ggatattgag gggacccgca cattcttccg	60
gactttcttc cgcttgccca catggatgtg gtgggggttt cttggatctt cgttatcatc	120
aactgacttg ataataatttg cgttttacat gtttatcata gcaccgcata gcctgagaat	180
gggtctggtt agacatttgc tttctgacct gacaggagga acaatgttaa aagcgtatct	240
cacgatataa ataactctag tcgcgatcag tttagattat aggcacatct tgcatatata	300
tatgtataaa ccttatgtgt gctgtatcct tacatcaaca cagtcattaa ttgtatttct	360
tggggtaatg ctgatgaagt attttctgtc gac	393

<210> 43

<211> 397

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<223> Antisense Fragment

<400> 43

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gaattctctt tggattagca ctgattgtcc agatggatat tgaggggacc cgcacattct    60
tccggacttt cttccgcttg cccacatgga tgtggtgggg gtttcttgga tcttcgttat    120
catcaactga cttgataata tttgcgtttt acatgtttat catagcaccg catagcctga    180
gaatgggtct ggttagacat ttgctttctg acccgacagg aggaacaatg ttaaaagcgt    240
atctcacgat ataaataact ctagtgcgga tcagttttaga ttataggcac atcttgcata    300
tatatatgta taaaccttat gtgtgctgta tccttacatc aacacagtca ttaattgtat    360
ttcttggggg aatgctgatg aagtattttc tggatcc                                397
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<210> 44

<211> 1537

<212> DNA

<213> Unknown

<220>

<221> promoter

<223> Promoter sequence

<400> 44

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gagctctaca aattagggtt actttattca ttttcacca ttctctttat tggttaaattt    60
tgtacattta ttcaataata ttatatgttt attacaaatt ctcactttct tattcatacc    120
tattcaactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt    180
tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaattgtcc    240
caaatttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt    300
aatacaaata aagtgaacaa aaatatctat aaataaacia atatatatat tttgttagac    360
gctgtctcaa cccatcaatt aaaaaatttt gttatatattc tactttacct actaaatttg    420
tttctcatat ttacctttta acccccacaa aaaaaatta taaaaaagaa agaaaaaagc    480
taaaccctat ttaaatagct aactataaga tcttaaaatt atcctcatca gtgtatagtt    540
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taattgggta ttaacttata acattatata tctatgacat atactctctc ctagctat	600
ctcacat	660
gctctaattt gattaacaaa aagttagaaa tattttattta aataaaaaag actaataaat	720
atataaaatg aatgttcata cgcagaccca tttagagatg agtatgcttt cacatgctga	780
gattat	840
aaattaacct gctcgtggtt gctgtatatg ggaggctaca aaataaatta aactaaagat	900
gattatggtt tagacat	960
cacaacccaa ttctat	1020
atattagggt ttattggact tttaatagta tcaaacaat ctatgtgtga acttaaaaat	1080
tgtattaaat atttagggtg acctggtgcc gtttttagaa taatg	1140
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gtctctgcct tctttgtata ttgtactccc cctcttcta tgccacgtgt tctgagctta	1260
acaagccacg ttgcgtgcca ttgccaaaca agtcatttta acttcacaag gtccgatttg	1320
acctccaaaa caacgacaag tttccgaaca gtcgcgaaga tcaagggtat aatcgtcttt	1380
ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt	1440
taaaacgtag ctgctgttta agtaaatccc agtccttcag tttgtgcttt tgtgtgtttt	1500
gtttctctga tttacggaat ttggaaataa taagctt	1537

<210> 45

<211> 734

<212> DNA

<213> Unknown

<220>

<221> variation

<223> synthetic sequence

<400> 45

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cctagggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc	120
cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cgggtggatcg	180
gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc	240
caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat	300

gatattttaga tagattagct atcacctgtg ctgtgggtgtg cagctcccaa gggctcttacc 360
gatagtaaaa tcgttagtta tgattaatac ttgggaggtg ggggattata ggctttgttg 420
tgagaatggt gagaaagagg ttgacaaat cgggtgtttga atgagggtta atggaggttta 480
attaaaataa agagaagaga aagattaaga gggatgatgg gatattaaag acggscaata 540
tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600
tggttgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660
ttgaatgcaa agcaaagcaa aggttgtttg ttgttgttgt tgagagacac tccaatccaa 720
acagatacaa ggcg 734

<210> 46

<211> 280

<212> DNA

<213> Unknown

<220>

<221> variation

<223> Synthetic sequence

<400> 46

gtcagagtatg gagttcaatt aaaataaaga gaagaraaag attaagaggg tgatggggat 60
attaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaac acatacaacg 120
tggttttaaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc 180
aaattcaatt caattctatt gaatgcaaag caaagcaaag caaagggttg ttgttggttg 240
tggtgagaga cactccaatc caaacagata caaggcgtga 280

<210> 47

<211> 358

<212> DNA

<213> Tagetes erecta

<220>

<221> Promoter

<223> Sense Promoter

<400> 47

aagcttaccg atagtaaaat cgtagttat gattaatact tgggaggtgg gggattatag 60
gctttgttg gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgagggttaa 120

tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga	180
cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa	240
aagatggctt ggctgctaata caactcaact caactcatat cctatccatt caaattcaat	300
tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtt tttgttggtt ttgtcgac	358

<210> 48

<211> 361

<212> DNA

<213> *Tagetes erecta*

<220>

<221> Promoter

<223> Antisense Promoter

<400> 48

ctcgagctta ccgatagtaa aatcgttagt tatgattaat acttgggagg tgggggatta	60
taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgaggtt	120
aaatggagtt taattaaaat aaagagaaga gaaagattaa gagggatgat gggatattaa	180
agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt	240
taaaagatgg cttggctgct aatcaactca actcaactca tatectatcc attcaaattc	300
aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttggttc	360
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<210> 49

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 49

gagctcactc actgatttcc attgcttg	28
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<210> 50

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 50

cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

37

<210> 51

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 51

atcaacggac atcgacttaa cggcgtttgt aaac

34

<210> 52

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 52

taagcttttt gttgaagaga tttgg

25

<210> 53

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 53

gaaaataactt catcagcatt acc

23

<210> 54
<211> 28
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<223> primer
<400> 54
gtcgactacg taagtttctg cttctacc 28

<210> 55
<211> 26
<212> DNA
<213> Artificial sequence
<220>
<223> primer
<400> 55
ggatccggtg atacctgcac atcaac 26

<210> 56
<211> 28
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<220>
<223> primer
<400> 56
aagcttgac gagggcaaagc aaagggtg 28

<210> 57
<211> 29
<212> DNA
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<400> 57
gtcgcacaacc aaatccagta tacagttac 29

<210> 58

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<400> 58
aggatccaac caaatccagt atacagttac 30

<210> 59

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<400> 59
gaattcgcac gaggc aaagc aaagggtg 28

<210> 60

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<212> DNA

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<400> 60
aagctttgga ttagcactga ttgtc 25

<210> 61

<211> 29

<212> DNA

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<220>

<223> primer

<400> 61

gtcgacagaa aatacttcat cagcattac

29

<210> 62

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 62

ggatccagaa aatacttcat cagcattac

29

<210> 63

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 63

gaattctctt tggattagca ctgattg

27

<210> 64

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 64

cgccttgtat ctgtttggat tgg

23

<210> 65

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 65

ctaacaatca atgagtatga gagc

24

<210> 66

<211> 26

<212> DNA

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<223> primer

<400> 66

agagcaaggc cagcaggacc acaacc

26

<210> 67

<211> 26

<212> DNA

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<223> primer

<400> 67

ccttgggagc ttttgggata ggctag

26

<210> 68

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 68

tcacgccttg tatctgtttg gattgg

26

<210> 69

<211> 15

<212> DNA

<213> Artificial sequence

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<400> 69

gtcgagtatg gagtt

15

<210> 70

<211> 28

<212> DNA

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<223> primer

<400> 70

aagcttaccg atagtaaaat cgttagtt

28

<210> 71

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 71

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31

<210> 72

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic sequence

<400> 72

gtcgacaaca acaacaaaca acctttgc

28

<210> 73

<211> 28

<212> DNA

<213> Artificial sequence

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<223> primer

<400> 73

ggatccaaca acaacaaaca acctttgc

28

<210> 74

<211> 28

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<223> primer

<400> 74

gtcgactttt tggtgaagag atttggtg

28

<210> 75

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 75

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28

<210> 76

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 76

gagctctaca aattaggggtt ac

22

<210> 77

<211> 23

<212> DNA

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<223> primer

<400> 77

aagcttatta tttccaaatt ccg

23

<210> 78

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 78

aagcttttgca attcatacag aagtgagaaa aatgcagcta gcagcgacag

50

<210> 79

<211> 1062

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (32) .. (1021)

<400> 79

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Met Gln Leu Ala Ala Thr Val

52

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Met	Leu	Glu	Gln	Leu	Thr	Gly	Ser	Ala	Glu	Ala	Leu	Lys	Glu	Lys	Glu	
	10						15					20				
aag	gag	gtt	gca	ggc	agc	tct	gac	gtg	ttg	cgt	aca	tgg	gcg	acc	cag	148
Lys	Glu	Val	Ala	Gly	Ser	Ser	Asp	Val	Leu	Arg	Thr	Trp	Ala	Thr	Gln	
	25					30					35					
tac	tcg	ctt	ccg	tca	gag	gag	tca	gac	gcg	gcc	cgc	ccg	gga	ctg	aag	196
Tyr	Ser	Leu	Pro	Ser	Glu	Glu	Ser	Asp	Ala	Ala	Arg	Pro	Gly	Leu	Lys	
40					45				50					55		
aat	gcc	tac	aag	cca	cca	cct	tcc	gac	aca	aag	ggc	atc	aca	atg	gcg	244
Asn	Ala	Tyr	Lys	Pro	Pro	Pro	Ser	Asp	Thr	Lys	Gly	Ile	Thr	Met	Ala	
				60					65					70		
cta	gct	gtc	atc	ggc	tcc	tgg	gcc	gca	gtg	ttc	ctc	cac	gcc	att	ttt	292
Leu	Ala	Val	Ile	Gly	Ser	Trp	Ala	Ala	Val	Phe	Leu	His	Ala	Ile	Phe	
			75				80						85			
caa	atc	aag	ctt	ccg	acc	tcc	ttg	gac	cag	ctg	cac	tgg	ctg	ccc	gtg	340
Gln	Ile	Lys	Leu	Pro	Thr	Ser	Leu	Asp	Gln	Leu	His	Trp	Leu	Pro	Val	
	90						95					100				
tca	gat	gcc	aca	gct	cag	ctg	gtt	agc	ggc	agc	agc	agc	ctg	ctg	cac	388
Ser	Asp	Ala	Thr	Ala	Gln	Leu	Val	Ser	Gly	Ser	Ser	Ser	Leu	Leu	His	
	105					110					115					
atc	gtc	gta	gta	ttc	ttt	gtc	ctg	gag	ttc	ctg	tac	aca	ggc	ctt	ttt	436
Ile	Val	Val	Val	Phe	Phe	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	
120					125					130					135	
atc	acc	acg	cat	gat	gct	atg	cat	ggc	acc	atc	gcc	atg	aga	aac	agg	484
Ile	Thr	Thr	His	Asp	Ala	Met	His	Gly	Thr	Ile	Ala	Met	Arg	Asn	Arg	
				140					145					150		
cag	ctt	aat	gac	ttc	ttg	ggc	aga	gta	tgc	atc	tcc	ttg	tac	gcc	tgg	532
Gln	Leu	Asn	Asp	Phe	Leu	Gly	Arg	Val	Cys	Ile	Ser	Leu	Tyr	Ala	Trp	
			155					160					165			
ttt	gat	tac	aac	atg	ctg	cac	cgc	aag	cat	tgg	gag	cac	cac	aac	cac	580
Phe	Asp	Tyr	Asn	Met	Leu	His	Arg	Lys	His	Trp	Glu	His	His	Asn	His	
	170						175					180				
act	ggc	gag	gtg	ggc	aag	gac	cct	gac	ttc	cac	agg	gga	aac	cct	ggc	628
Thr	Gly	Glu	Val	Gly	Lys	Asp	Pro	Asp	Phe	His	Arg	Gly	Asn	Pro	Gly	
	185					190					195					
att	gtg	ccc	tgg	ttt	gcc	agc	ttc	atg	tcc	agc	tac	atg	tcg	atg	tgg	676
Ile	Val	Pro	Trp	Phe	Ala	Ser	Phe	Met	Ser	Ser	Tyr	Met	Ser	Met	Trp	
200					205					210					215	
cag	ttt	gcg	cgc	ctc	gca	tgg	tgg	acg	gtg	gtc	atg	cag	ctg	ctg	ggt	724
Gln	Phe	Ala	Arg	Leu	Ala	Trp	Trp	Thr	Val	Val	Met	Gln	Leu	Leu	Gly	
				220					225					230		
gcg	cca	atg	gcg	aac	ctg	ctg	gtg	ttc	atg	gcg	gcc	gcg	ccc	atc	ctg	772
Ala	Pro	Met	Ala	Asn	Leu	Leu	Val	Phe	Met	Ala	Ala	Ala	Pro	Ile	Leu	

235	240	245	
tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc cac aag cct			820
Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro His Lys Pro			
250	255	260	
gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg aac tgg tgg			868
Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met Asn Trp Trp			
265	270	275	
aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt ctg acc tgc			916
Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe Leu Thr Cys			
280	285	290	295
tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc ttt gcc ccc			964
Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro			
300	305	310	
tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga ggt ctg gtt			1012
Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg Gly Leu Val			
315	320	325	
cct gcc tag ctggacacac tgcagtgggc cctgctgccca gctgggcatg c			1062
Pro Ala			

<210> 80

<211> 329

<212> PRT

<213> Haematococcus pluvialis

<400> 80

Met	Gln	Leu	Ala	Ala	Thr	Val	Met	Leu	Glu	Gln	Leu	Thr	Gly	Ser	Ala
1				5					10					15	

Glu	Ala	Leu	Lys	Glu	Lys	Glu	Lys	Glu	Val	Ala	Gly	Ser	Ser	Asp	Val
		20						25					30		

Leu	Arg	Thr	Trp	Ala	Thr	Gln	Tyr	Ser	Leu	Pro	Ser	Glu	Glu	Ser	Asp
	35					40					45				

Ala	Ala	Arg	Pro	Gly	Leu	Lys	Asn	Ala	Tyr	Lys	Pro	Pro	Pro	Ser	Asp
50					55					60					

Thr	Lys	Gly	Ile	Thr	Met	Ala	Leu	Ala	Val	Ile	Gly	Ser	Trp	Ala	Ala
65				70					75					80	

Val	Phe	Leu	His	Ala	Ile	Phe	Gln	Ile	Lys	Leu	Pro	Thr	Ser	Leu	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala

325

<210> 81

<211> 789

<212> DNA

<213> Nostoc punctiforme

<220>

<221> CDS

<400> 81

ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa	48
Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln	
1 5 10 15	
tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta	96
Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val	
20 25 30	
att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat	144
Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn	
35 40 45	
tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa	192
Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln	
50 55 60	
atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat	240
Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His	
65 70 75 80	
ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca	288
Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser	
85 90 95	
cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag	336
Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys	
100 105 110	
aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat	384
Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp	
115 120 125	
ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc	432
Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe	
130 135 140	
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta	480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu	
145 150 155 160	
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc	528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile	

165	170	175	
tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat			576
Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr			
180	185	190	
ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat			624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr			
195	200	205	
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc			672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
210	215	220	
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat			720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
225	230	235	240
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac			768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn			
245	250	255	
aat tca gta acc aat tcg taa			789
Asn Ser Val Thr Asn Ser			
260			
<210>	82		
<211>	262		
<212>	PRT		
<213>	Nostoc punctiforme		
<400>	82		
Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln			
1	5	10	15
Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val			
20	25	30	
Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn			
35	40	45	
Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln			
50	55	60	
Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His			
65	70	75	80
Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser			
85	90	95	

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255

Asn Ser Val Thr Asn Ser
 260

<210> 83

<211> 762

<212> DNA

<213> Nostoc punctiforme

<220>

<221> CDS

<400> 83

gtg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca
 Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro

1	5	10	15	
gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc				96
Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val				
20	25	30		
att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac				144
Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp				
35	40	45		
atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa				192
Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln				
50	55	60		
aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat				240
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His				
65	70	75	80	
ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca				288
Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr				
85	90	95		
ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa				336
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys				
100	105	110		
aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat				384
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp				
115	120	125		
ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt				432
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe				
130	135	140		
atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att				480
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile				
145	150	155	160	
tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act				528
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr				
165	170	175		
tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat				576
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr				
180	185	190		
ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag				624
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln				
195	200	205		
cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc				672
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile				
210	215	220		
acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat				720
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His				
225	230	235	240	
att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag				762
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys				

245

250

<210> 84

<211> 253

<212> PRT

<213> Nostoc punctiforme

<400> 84

Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
 1 5 10 15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
 35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
 100 105 110

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
 115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
 130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
 165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr

180

185

190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> 85

<211> 804

<212> DNA

<213> Synechococcus WH8102

<220>

<221> CDS

<400> 85

atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac 48
 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
 1 5 10 15

cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96
 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30

ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
 35 40 45

tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg 192
 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
 50 55 60

ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg 240
 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu
 65 70 75 80

ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat 288
 Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
 85 90 95

ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca 336
 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
 100 105 110

ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg 384
 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu
 115 120 125
 gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac 432
 Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
 130 135 140
 aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg 480
 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
 145 150 155 160
 cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc 528
 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
 165 170 175
 aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc 576
 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
 180 185 190
 gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc 624
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
 195 200 205
 tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg 672
 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
 210 215 220
 cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac 720
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240
 ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt 768
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
 245 250 255
 cag ctg cca caa ctt cga aat gaa tca ttc act tga 804
 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
 260 265

<210> 86

<211> 267

<212> PRT

<213> Synechococcus WH8102

<400> 86

Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
 1 5 10 15

Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30

Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu

35

40

45

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
50 55 60

Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu
65 70 75 80

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
85 90 95

Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
100 105 110

Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu
115 120 125

Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
145 150 155 160

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
165 170 175

Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
180 185 190

Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
195 200 205

Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
210 215 220

Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
225 230 235 240

Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
245 250 255

Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
260 265

<211> 33

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 87

gcatgctcta gaccttataa agatattttg tga

33

<210> 88

<211> 33

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 88

gcatgcatct agaaatgggt cagtgtcaac cat

33

<210> 89

<211> 805

<212> DNA

<213> Nostoc sp. Strain PCC7120

<220>

<221> variation

<400> 89

gcatgcatct agaaatgggt cagtgtcaac catcatctct gcattcagaa aaactgggtgt

60

tattgtcatc gacaatcaga gatgataaaa atattaataa gggatatattt attgcctgct

120

ttatcttatt tttatgggca attagtttaa tcttattact ctcaatagat acatccataa

180

ttcataagag cttattaggt atagccatgc tttggcagac cttcttatat acagggtttat

240

ttattactgc tcatgatgcc atgcacggcg tagtttatcc caaaaatccc agaataaata

300

attttatagg taagctcact ctaatcttgt atggactact cccttataaa gattttattga 360
 aaaaacattg gttacaccac ggacatcctg gtactgattt agaccctgat tattacaatg 420
 gtcaccccca aaacttcttt ctttggtatc tacattttat gaagtcttat tggcgatgga 480
 cgcaaatttt cggattagtg atgatttttc atggacttaa aaatctggtg catataccag 540
 aaaataattt aatttatattt tggatgatac cttctatttt aagttcagta caactatttt 600
 attttggtac atttttgcct cataaaaagc tagaagggtg ttataactaac cccattgtg 660
 cgcgcagtat cccattacct cttttttggt cttttgttac ttgttatcac ttcggctacc 720
 acaaggaaca tcacgaatac cctcaacttc cttggtggaa attacctgaa gctcacaaaa 780
 tatctttata aggtctagag catgc 805

<210> 90

<211> 35

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 90

gagctcttca ttatttcgat tttgatttcg tgacc 35

<210> 91

<211> 44

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 91

aagcttgagc tcggttgatc agaagaagaa gaagaagatg aact 44

<210> 92

<211> 653

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> promoter

<400> 92

gagctcttca ttatttcgat tttgatttcg tgaccagcga acgcagaata ccttgttgtg	60
taataacttta cccgtgtaaa tcaaaaacaa aaaggctttt gagctttttg tagttgaatt	120
tctctggctg atctttttctg tacagattca tatatctgca gagacgatat cattgattat	180
ttgagcttct tttgaactat ttctgtgaat ttgggatgag agctctatgt atgtgtgtaa	240
actttgaaga caacaagaaa ggtaacaagt gagggaggga tgactccatg tcaaaataga	300
tgtcataaga ggcccatcaa taagtgcttg agcccattag ctagcccagt aactaccaga	360
ttgtgagatg gatgtgtgaa cagttttttt ttgatgtag gactgaaatg tgaacaacag	420
g'gcgatgaaa ggctaaatta ggacaatgat aagcagaaat aacttatcct ctctaact	480
tggcctcaca ttgcccttca cacaatccac acacatccaa tcacaacctc atcatatatc	540
tcccgtaat ctttttttct ttgatctttt tttttttgct tattattttt ttgactttga	600
tctcccatca gttcatcttc ttctttctct tctgatcaac cgagctcaag ctt	653

<210> 93

<211> 28

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 93

gagctcactc actgatttcc attgcttg	28
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<210> 94

<211> 30

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 94

aagcttgagc tctttgttga agagatttgg

30

<210> 95

<211> 37

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 95

cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

37

<210> 96

<211> 34

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Synthetic sequence

<400> 96

atcaacggac atcgacttaa cggcgtttgt aaac

34

<210> 97

<211> 831

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<400> 97

atg cca tcc gag tcg tca gac gca gct cgt cct gtg ttg aag cac gcc
Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala
1 5 10 15

48

tat	aaa	cct	cca	gca	tct	gac	gcc	aag	ggc	atc	act	atg	gcg	ctg	acc	96
Tyr	Lys	Pro	Pro	Ala	Ser	Asp	Ala	Lys	Gly	Ile	Thr	Met	Ala	Leu	Thr	
		20						25					30			
atc	att	ggc	acc	tgg	acc	gca	gtg	ttt	tta	cac	gca	ata	ttc	caa	atc	144
Ile	Ile	Gly	Thr	Trp	Thr	Ala	Val	Phe	Leu	His	Ala	Ile	Phe	Gln	Ile	
		35					40					45				
agg	cta	ccg	aca	tcc	atg	gac	cag	ctt	cac	tgg	ttg	cct	gtg	tcc	gaa	192
Arg	Leu	Pro	Thr	Ser	Met	Asp	Gln	Leu	His	Trp	Leu	Pro	Val	Ser	Glu	
	50					55					60					
gcc	aca	gcc	cag	ctg	ttg	ggc	gga	agc	agc	agc	cta	ttg	cac	atc	gcc	240
Ala	Thr	Ala	Gln	Leu	Leu	Gly	Gly	Ser	Ser	Ser	Leu	Leu	His	Ile	Ala	
65					70					75					80	
gca	gtc	ttc	att	gta	ctt	gag	ttt	ctg	tac	act	ggg	cta	ttc	atc	acc	288
Ala	Val	Phe	Ile	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	
			85					90						95		
acg	cat	gat	gca	atg	cat	ggc	acc	ata	gct	ttg	agg	aac	agg	cag	ctc	336
Thr	His	Asp	Ala	Met	His	Gly	Thr	Ile	Ala	Leu	Arg	Asn	Arg	Gln	Leu	
			100					105					110			
aat	gat	ctc	ctt	ggc	aac	atc	tgc	ata	tca	ctg	tac	gcc	tgg	ttt	gac	384
Asn	Asp	Leu	Leu	Gly	Asn	Ile	Cys	Ile	Ser	Leu	Tyr	Ala	Trp	Phe	Asp	
		115					120					125				
tac	agc	atg	cac	tgg	gag	cac	cac	aac	cat	act	ggc	gaa	gtg	ggg	aaa	432
Tyr	Ser	Met	His	Trp	Glu	His	His	Asn	His	Thr	Gly	Glu	Val	Gly	Lys	
	130					135					140					
gac	cct	gac	ttc	cac	aaa	gga	aat	cct	ggc	ctt	gtc	ccc	tgg	ttc	gcc	480
Asp	Pro	Asp	Phe	His	Lys	Gly	Asn	Pro	Gly	Leu	Val	Pro	Trp	Phe	Ala	
145					150					155					160	
agc	ttc	atg	tcc	agc	tac	atg	tcc	ctg	tgg	cag	ttt	gcc	cgg	ctg	gca	528
Ser	Phe	Met	Ser	Ser	Tyr	Met	Ser	Leu	Trp	Gln	Phe	Ala	Arg	Leu	Ala	
			165					170						175		
tgg	tgg	gca	gtg	gtg	atg	caa	acg	ttg	ggg	gcc	ccc	atg	gcg	aat	ctc	576
Trp	Trp	Ala	Val	Val	Met	Gln	Thr	Leu	Gly	Ala	Pro	Met	Ala	Asn	Leu	
			180					185					190			
cta	gtc	ttc	atg	gct	gca	gcc	cca	atc	ttg	tca	gca	ttc	cgc	ctc	ttc	624
Leu	Val	Phe	Met	Ala	Ala	Ala	Pro	Ile	Leu	Ser	Ala	Phe	Arg	Leu	Phe	
		195					200					205				
tac	ttc	ggc	act	tac	ctg	cca	cac	aag	cct	gag	cca	ggc	cct	gca	gca	672
Tyr	Phe	Gly	Thr	Tyr	Leu	Pro	His	Lys	Pro	Glu	Pro	Gly	Pro	Ala	Ala	
	210					215					220					
ggc	tct	cag	gtc	atg	tct	tgg	ttc	agg	gcc	aag	aca	agt	gag	gca	tct	720
Gly	Ser	Gln	Val	Met	Ser	Trp	Phe	Arg	Ala	Lys	Thr	Ser	Glu	Ala	Ser	
225					230					235					240	
gat	gtg	atg	agc	ttc	ctg	aca	tgc	tac	cac	ttt	gac	ctg	ttt	gcc	ccc	768
Asp	Val	Met	Ser	Phe	Leu	Thr	Cys	Tyr	His	Phe	Asp	Leu	Phe	Ala	Pro	
			245						250					255		

tgg tgg cag ctg ccc cac tgc cgc cgc ctg tct ggg cgt ggc ctg gtg 816
 Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 260 265 270

cct gcc ttg gca tga 831
 Pro Ala Leu Ala
 275

<210> 98

<211> 276

<212> PRT

<213> Haematococcus pluvialis

<400> 98

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala
 1 5 10 15

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
 20 25 30

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
 35 40 45

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
 50 55 60

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
 65 70 75 80

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
 85 90 95

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu
 100 105 110

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
 115 120 125

Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys
 130 135 140

Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala
 145 150 155 160

Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala

165

170

175

Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu
 180 185 190

Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe
 195 200 205

Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala
 210 215 220

Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser
 225 230 235 240

Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro
 245 250 255

Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 260 265 270

Pro Ala Leu Ala
 275

<210> 99

<211> 729

<212> DNA

<213> Paracoccus sp. MBIC1143

<220>

<221> CDS

<400> 99

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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca 144
 Ala Leu Trp Phe Leu Asp Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	
gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
145 150 155 160	
gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
180 185 190	
gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg	624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	
195 200 205	
ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac	672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His	
210 215 220	
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac	720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp	
225 230 235 240	
acc gca tga	729
Thr Ala	

<210> 100

<211> 242

<212> PRT

<213> Paracoccus sp. MBIC1143

<400> 100

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu

1	5	10	15
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	20	25	30
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	35	40	45
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	50	55	60
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	65	70	75
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	85	90	95
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	100	105	110
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	115	120	125
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	130	135	140
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	145	150	155
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	165	170	175
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	180	185	190
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	195	200	205
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His	210	215	220
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp	225	230	235
Thr Ala			

<210> 101

<211> 735

<212> DNA

<213> Brevundimonas aurantiaca

<220>

<221> CDS

<400> 101

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Met	Thr	Ala	Ala	Val	Ala	Glu	Pro	Arg	Thr	Val	Pro	Arg	Gln	Thr	Trp	
1				5					10					15		

atc	ggt	ctg	acc	ctg	gcg	gga	atg	atc	gtg	gcg	gga	tgg	gcg	gtt	ctg	96
Ile	Gly	Leu	Thr	Leu	Ala	Gly	Met	Ile	Val	Ala	Gly	Trp	Ala	Val	Leu	
			20					25					30			

cat	gtc	tac	ggc	gtc	tat	ttt	cac	cga	tgg	ggg	ccg	ttg	acc	ctg	gtg	144
His	Val	Tyr	Gly	Val	Tyr	Phe	His	Arg	Trp	Gly	Pro	Leu	Thr	Leu	Val	
		35					40					45				

atc	gcc	ccg	gcg	atc	gtg	gcg	gtc	cag	acc	tgg	ttg	tcg	gtc	ggc	ctt	192
Ile	Ala	Pro	Ala	Ile	Val	Ala	Val	Gln	Thr	Trp	Leu	Ser	Val	Gly	Leu	
	50					55					60					

ttc	atc	gtc	gcc	cat	gac	gcc	atg	tac	ggc	tcc	ctg	gcg	ccg	gga	cgg	240
Phe	Ile	Val	Ala	His	Asp	Ala	Met	Tyr	Gly	Ser	Leu	Ala	Pro	Gly	Arg	
65				70					75					80		

ccg	cgg	ctg	aac	gcc	gca	gtc	ggc	cgg	ctg	acc	ctg	ggg	ctc	tat	gcg	288
Pro	Arg	Leu	Asn	Ala	Ala	Val	Gly	Arg	Leu	Thr	Leu	Gly	Leu	Tyr	Ala	
			85					90					95			

ggc	ttc	cgc	ttc	gat	cgg	ctg	aag	acg	gcg	cac	cac	gcc	cac	cac	gcc	336
Gly	Phe	Arg	Phe	Asp	Arg	Leu	Lys	Thr	Ala	His	His	Ala	His	His	Ala	
			100					105					110			

gcg	ccc	ggc	acg	gcc	gac	gac	ccg	gat	ttt	cac	gcc	ccg	gcg	ccc	cgc	384
Ala	Pro	Gly	Thr	Ala	Asp	Asp	Pro	Asp	Phe	His	Ala	Pro	Ala	Pro	Arg	
		115					120					125				

gcc	ttc	ctt	ccc	tgg	ttc	ctg	aac	ttc	ttt	cgc	acc	tat	ttc	ggc	tgg	432
Ala	Phe	Leu	Pro	Trp	Phe	Leu	Asn	Phe	Phe	Arg	Thr	Tyr	Phe	Gly	Trp	
		130				135					140					

cgc	gag	atg	gcg	gtc	ctg	acc	gcc	ctg	gtc	ctg	atc	gcc	ctc	ttc	ggc	480
Arg	Glu	Met	Ala	Val	Leu	Thr	Ala	Leu	Val	Leu	Ile	Ala	Leu	Phe	Gly	
145				150					155					160		

ctg	ggg	gcg	cgg	ccg	gcc	aat	ctc	ctg	acc	ttc	tgg	gcc	gcg	ccg	gcc	528
Leu	Gly	Ala	Arg	Pro	Ala	Asn	Leu	Leu	Thr	Phe	Trp	Ala	Ala	Pro	Ala	
				165				170						175		

ctg ctt tca gcg ctt cag ctc ttc acc ttc ggc acc tgg ctg ccg cac 576
 Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His
 180 185 190

cgc cac acc gac cag ccg ttc gcc gac gcg cac cac gcc cgc agc agc 624
 Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
 195 200 205

ggc tac ggc ccc gtg ctt tcc ctg ctc acc tgt ttc cac ttc ggc cgc 672
 Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
 210 215 220

cac cac gaa cac cat ctg agc ccc tgg cgg ccc tgg tgg cgt ctg tgg 720
 His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp
 225 230 235 240

cgc ggc gag tct tga 735
 Arg Gly Glu Ser

<210> 102

<211> 244

<212> PRT

<213> Brevundimonas aurantiaca

<400> 102

Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp
 1 5 10 15

Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu
 20 25 30

His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val
 35 40 45

Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu
 50 55 60

Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg
 65 70 75 80

Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala
 85 90 95

Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala
 100 105 110

Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg

115

120

125

Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp
 130 135 140

Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly
 145 150 155 160

Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala
 165 170 175

Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His
 180 185 190

Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
 195 200 205

Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
 210 215 220

His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp
 225 230 235 240

Arg Gly Glu Ser

<210> 103

<211> 690

<212> DNA

<213> Nodularia spumigena NSOR10

<220>

<221> CDS

<400> 103

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 1 5 10 15

ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc 96
 Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30

ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat 144
 Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45

gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat	192
Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His	
50 55 60	
ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa	240
Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln	
65 70 75 80	
aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa	288
Lys Leu Leu Lys Lys His Trp Leu His His Asn Pro Ala Ser Glu	
85 90 95	
aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg	336
Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp	
100 105 110	
tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca	384
Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr	
115 120 125	
tta atg att att tat aac tta cta aaa tat ata tgg cat ttt cca gag	432
Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu	
130 135 140	
gat aat atg act tat ttt tgg gta gtt ccc tca att tta agt tct tta	480
Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu	
145 150 155 160	
caa tta ttt tat ttt gga act ttt cta ccc cac agt gag cct gta gaa	528
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu	
165 170 175	
ggg tat aaa gag cct cat cgt tcc caa act att agc cgt ccc att tgg	576
Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp	
180 185 190	
tgg tca ttt ata act tgt tac cat ttt ggt tat cat tac gaa cat cat	624
Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His	
195 200 205	
gaa tac ccc cat gtt cct tgg tgg caa tta cca gaa att tat aaa atg	672
Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met	
210 215 220	
tct aaa tca aat ttg tga	690
Ser Lys Ser Asn Leu	
225	

<210> 104

<211> 229

<212> PRT

<213> Nodularia spumigena NSOR10

<400> 104

Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu

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Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu	20	25	30
Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His	35	40	45
Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His	50	55	60
Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln	65	70	75
Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu	85	90	95
Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp	100	105	110
Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr	115	120	125
Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu	130	135	140
Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu	145	150	155
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu	165	170	175
Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp	180	185	190
Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His	195	200	205
Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met	210	215	220
Ser Lys Ser Asn Leu	225		

<210> 105

<211> 1536

<212> DNA

<213> Deinococcus radiodurans R1

<220>

<221> CDS

<400> 105

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gtg act gct gcc tac gcc gcc cgg gcg ggc ctg aaa gtc ggc gtg ttc	96
Val Thr Ala Ala Tyr Ala Ala Arg Ala Gly Leu Lys Val Gly Val Phe	
20 25 30	
gag cgg cgg cac ctc gtc ggc ggg gcg gtc agc acc gag gag gtc gtg	144
Glu Arg Arg His Leu Val Gly Gly Ala Val Ser Thr Glu Glu Val Val	
35 40 45	
ccc ggt tac cgc ttc gac tac ggc ggc agc gcc cac atc ctg att cgg	192
Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg	
50 55 60	
atg acg ccc atc gtg cgc gaa ctc gaa ctc acg cgg cac ggg ctg cat	240
Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His	
65 70 75 80	
tac ctc gaa gtg gac cct atg ttt cac gct tcc gac ggt gaa acg ccc	288
Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro	
85 90 95	
tgg ttc att cac cgc gac gcc ggg cgg acc atc cgc gaa ctg gac gaa	336
Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu	
100 105 110	
aag ttt ccc ggg cag ggc gac gcc tac ggg cgc ttt ctc gac gat tgg	384
Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp	
115 120 125	
aca ccc ttc gcg cgc gcc gtg gcc gac ctg ttc aac tcg gcg ccg ggg	432
Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly	
130 135 140	
ccg ctc gac ctg ggc aaa atg gtg atg cgc agc ggc cag ggc aag gac	480
Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp	
145 150 155 160	
tgg aac gag cag ctc ccg cgc atc ctg cgg ccc tac ggc gac gtg gcg	528
Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala	
165 170 175	
cgc gag tac ttc agc gag gag cgc gtg cgg gct ccc ctg acc tgg atg	576
Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met	
180 185 190	

gcg gcc cag agc ggc ccc cca ccc tcg gac ccg ctg agc gcg ccc ttt Ala Ala Gln Ser Gly Pro Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe 195 200 205	624
ttg ctg tgg cac ccg ctc tac cac gaa ggc ggc gtg gcg cgg ccc aaa Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys 210 215 220	672
ggc ggc agc ggc ggc ctg acc aaa gcc ctg cgc cgg gcc acc gag gcc Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala 225 230 235 240	720
gaa ggc ggc gag gtc ttc acc gac gcg ccg gtc aag gaa att ctg gtc Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val 245 250 255	768
aag gac ggc aag gcg cag ggc atc cgg ctg gaa agc ggc gag acg tac Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr 260 265 270	816
acc gcc cgc gcc gtc gtg tcg ggc gtc cac atc ctg acc act gcg aat Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn 275 280 285	864
gcc ctg ccc gcc gaa tat gtc cct agc gcc gcc agg aat gtg cgc gtg Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val 290 295 300	912
ggc aac ggc ttc ggc atg att ttg cgc ctc gcc ctc agt gaa aaa gtc Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val 305 310 315 320	960
aaa tac cgt cac cac acc gag ccc gac tca cgc atc ggc ctg gga ttg Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu 325 330 335	1008
ctg atc aaa aac gag cgg caa atc atg cag ggc tac ggc gaa tac ctc Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu 340 345 350	1056
gcc ggg cag ccc acc acc gac ccg ccc ctc gtc gcc atg agc ttc agc Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser 355 360 365	1104
gcg gtg gac gac tcg ctc gcc cca ccg aac ggc gac gtg ttg tgg ctg Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu 370 375 380	1152
tgg gcg cag tac tac ccc ttc gag ctc gcc acc ggg agc tgg gaa acg Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr 385 390 395 400	1200
cgc acc gcc gaa gcg cgg gag aac atc ctg cgg gcc ttt gag cac tac Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr 405 410 415	1248
gcg ccg ggc acc cgc gac acg att gtg ggc gaa ctc gtg cag acg ccg Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro 420 425 430	1296

cag tgg ctg gaa acc aac ctc ggc ctg cac cgg ggc aac gtg atg cac 1344
 Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His
 435 440 445

ctg gaa atg tcc ttc gac cag atg ttc tcc ttc cgc ccc tgg ctg aaa 1392
 Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys
 450 455 460

gcg agc cag tac cgc tgg ccg ggc gtg cag ggg ctg tac ctc acc ggc 1440
 Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly
 465 470 475 480

gcc agc acc cac ccc ggc gga ggc atc atg ggc gcc tcg gga cgc aac 1488
 Ala Ser Thr His Pro Gly Gly Gly Ile Met Gly Ala Ser Gly Arg Asn
 485 490 495

gcg gcg cgg gtc atc gtg aag gac ctg acg cgg agg cgc tgg aaa tga 1536
 Ala Ala Arg Val Ile Val Lys Asp Leu Thr Arg Arg Arg Trp Lys
 500 505 510

<210> 106

<211> 511

<212> PRT

<213> Deinococcus radiodurans R1

<400> 106

Met Pro Asp Tyr Asp Leu Ile Val Met Gly Ala Gly His Asn Ala Leu
 1 5 10 15

Val Thr Ala Ala Tyr Ala Ala Arg Ala Gly Leu Lys Val Gly Val Phe
 20 25 30

Glu Arg Arg His Leu Val Gly Gly Ala Val Ser Thr Glu Glu Val Val
 35 40 45

Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg
 50 55 60

Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His
 65 70 75 80

Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro
 85 90 95

Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu
 100 105 110

Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp

115	120	125
Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly		
130	135	140
Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp		
145	150	155
Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala		
	165	170
Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met		
	180	185
Ala Ala Gln Ser Gly Pro Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe		
	195	200
Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys		
	210	215
Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala		
225	230	235
Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val		
	245	250
Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr		
	260	265
Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn		
	275	280
Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val		
	290	295
Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val		
305	310	315
Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu		
	325	330
Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu		
	340	345
Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser		

355

360

365

Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu
 370 375 380

Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr
 385 390 395 400

Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr
 405 410 415

Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro
 420 425 430

Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His
 435 440 445

Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys
 450 455 460

Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly
 465 470 475 480

Ala Ser Thr His Pro Gly Gly Gly Ile Met Gly Ala Ser Gly Arg Asn
 485 490 495

Ala Ala Arg Val Ile Val Lys Asp Leu Thr Arg Arg Arg Trp Lys
 500 505 510

<210> 107

<211> 1666

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (1)..(1494)

<400> 107

atg gaa gct ctt ctc aag cct ttt cca tct ctt tta ctt tcc tct cct 48
 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
 1 5 10 15

aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc 96
 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro

20					25					30						
acc	acc	aaa	aaa	aaa	tca	aga	aaa	tgt	ctt	ctt	aga	aac	aaa	agt	agt	144
Thr	Thr	Lys	Lys	Lys	Ser	Arg	Lys	Cys	Leu	Leu	Arg	Asn	Lys	Ser	Ser	
		35					40				45					
aaa	ctt	ttt	tgt	agc	ttt	ctt	gat	tta	gca	ccc	aca	tca	aag	cca	gag	192
Lys	Leu	Phe	Cys	Ser	Phe	Leu	Asp	Leu	Ala	Pro	Thr	Ser	Lys	Pro	Glu	
	50					55					60					
tct	tta	gat	gtt	aac	atc	tca	tgg	gtt	gat	cct	aat	tcg	aat	cgg	gct	240
Ser	Leu	Asp	Val	Asn	Ile	Ser	Trp	Val	Asp	Pro	Asn	Ser	Asn	Arg	Ala	
65					70					75					80	
caa	ttc	gac	gtg	atc	att	atc	gga	gct	ggc	cct	gct	ggg	ctc	agg	cta	288
Gln	Phe	Asp	Val	Ile	Ile	Ile	Gly	Ala	Gly	Pro	Ala	Gly	Leu	Arg	Leu	
				85				90						95		
gct	gaa	caa	gtt	tct	aaa	tat	ggg	att	aag	gta	tgt	tgt	gtt	gac	cct	336
Ala	Glu	Gln	Val	Ser	Lys	Tyr	Gly	Ile	Lys	Val	Cys	Cys	Val	Asp	Pro	
			100				105						110			
tca	cca	ctc	tcc	atg	tgg	cca	aat	aat	tat	ggg	gtt	tgg	gtt	gat	gag	384
Ser	Pro	Leu	Ser	Met	Trp	Pro	Asn	Asn	Tyr	Gly	Val	Trp	Val	Asp	Glu	
		115				120						125				
ttt	gag	aat	tta	gga	ctg	gaa	aat	tgt	tta	gat	cat	aaa	tgg	cct	atg	432
Phe	Glu	Asn	Leu	Gly	Leu	Glu	Asn	Cys	Leu	Asp	His	Lys	Trp	Pro	Met	
	130					135					140					
act	tgt	gtg	cat	ata	aat	gat	aac	aaa	act	aag	tat	ttg	gga	aga	cca	480
Thr	Cys	Val	His	Ile	Asn	Asp	Asn	Lys	Thr	Lys	Tyr	Leu	Gly	Arg	Pro	
145					150					155					160	
tat	ggg	aga	gtt	agt	aga	aag	aag	ctg	aag	ttg	aaa	ttg	ttg	aat	agt	528
Tyr	Gly	Arg	Val	Ser	Arg	Lys	Lys	Leu	Lys	Leu	Lys	Leu	Leu	Asn	Ser	
				165				170						175		
tgt	gtt	gag	aac	aga	gtg	aag	ttt	tat	aaa	gct	aag	gtt	tgg	aaa	gtg	576
Cys	Val	Glu	Asn	Arg	Val	Lys	Phe	Tyr	Lys	Ala	Lys	Val	Trp	Lys	Val	
			180					185					190			
gaa	cat	gaa	gaa	ttt	gag	tct	tca	att	gtt	tgt	gat	gat	ggg	aag	aag	624
Glu	His	Glu	Glu	Phe	Glu	Ser	Ser	Ile	Val	Cys	Asp	Asp	Gly	Lys	Lys	
		195					200					205				
ata	aga	ggg	agt	ttg	gtt	gtg	gat	gca	agt	ggg	ttt	gct	agt	gat	ttt	672
Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe	
	210					215					220					
ata	gag	tat	gac	agg	cca	aga	aac	cat	ggg	tat	caa	att	gct	cat	ggg	720
Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly	
225					230					235					240	
gtt	tta	gta	gaa	gtt	gat	aat	cat	cca	ttt	gat	ttg	gat	aaa	atg	gtg	768
Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val	
				245					250					255		
ctt	atg	gat	tgg	agg	gat	tct	cat	ttg	ggg	aat	gag	cca	tat	tta	agg	816
Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg	

260	265	270	
gtg aat aat gct aaa gaa cca aca ttc ttg tat gca atg cca ttt gat Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp 275 280 285			864
aga gat ttg gtt ttc ttg gaa gag act tct ttg gtg agt cgt cct gtt Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val 290 295 300			912
tta tcg tat atg gaa gta aaa aga agg atg gtg gca aga tta agg cat Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His 305 310 315 320			960
ttg ggg atc aaa gtg aaa agt gtt att gag gaa gag aaa tgt gtg atc Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Lys Cys Val Ile 325 330 335			1008
cct atg gga gga cca ctt ccg cgg att cct caa aat gtt atg gct att Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile 340 345 350			1056
ggg ggg aat tca ggg ata gtt cat cca tca aca ggg tac atg gtg gct Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala 355 360 365			1104
agg agc atg gct tta gca cca gta cta gct gaa gcc atc gtc gag ggg Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly 370 375 380			1152
ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val 385 390 395 400			1200
tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr 405 410 415			1248
tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg 420 425 430			1296
aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly 435 440 445			1344
ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu 450 455 460			1392
tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr 465 470 475 480			1440
aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu 485 490 495			1488
agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat Ser Leu			1544

tttcatattt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaaact 1604
 actattggaa agttaaataa tgtgtttggt gtatgttatt ctaatggaat ggattttgta 1664
 aa 1666

<210> 108

<211> 498

<212> PRT

<213> Lycopersicon esculentum

<400> 108

Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
 1 5 10 15

Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
 20 25 30

Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
 35 40 45

Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
 50 55 60

Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
 65 70 75 80

Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
 85 90 95

Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
 100 105 110

Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
 115 120 125

Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
 130 135 140

Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
 145 150 155 160

Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Asn Ser

165	170	175
Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val		
180	185	190
Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys		
195	200	205
Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe		
210	215	220
Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly		
225	230	235 240
Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val		
245	250	255
Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg		
260	265	270
Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp		
275	280	285
Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val		
290	295	300
Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His		
305	310	315 320
Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile		
325	330	335
Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile		
340	345	350
Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala		
355	360	365
Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly		
370	375	380
Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val		
385	390	395 400
Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr		

405

410

415

Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
 420 425 430

Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
 435 440 445

Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
 450 455 460

Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
 465 470 475 480

Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu
 485 490 495

Ser Leu

<210> 109

<211> 1125

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (20) .. (946)

<400> 109

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Met Ala Ala Ala Ala Arg Ile Ser Ala Ser Ser
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acc tca cga act ttt tat ttc cgt cat tca ccg ttt ctt ggc cca aaa 100

Thr Ser Arg Thr Phe Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys
 15 20 25

cct act tcg aca acc tca cat gtt tct cca atc tct cct ttt tct ctt 148

Pro Thr Ser Thr Thr Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu
 30 35 40

aat cta ggc cca att ttg agg tct aga aga aaa ccc agt ttc act gtt 196

Asn Leu Gly Pro Ile Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val
 45 50 55

tgc ttt gtt ctc gag gat gag aag ctg aaa cct caa ttt gac gat gag 244

Cys Phe Val Leu Glu Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu

60	65	70	75	
gct gag gat ttt gaa aag aag att gag gaa cag atc tta gct act cgc				292
Ala Glu Asp Phe Glu Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg	80	85	90	
ttg gcg gag aaa ctg gct agg aag aaa tcg gag agg ttt act tat ctt				340
Leu Ala Glu Lys Leu Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu	95	100	105	
gtg gct gct ata atg tct agt ttt ggg att act tct atg gct gtt atg				388
Val Ala Ala Ile Met Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met	110	115	120	
gct gtt tat tac aga ttt tcg tgg caa atg gag gga gga gaa gtt cct				436
Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro	125	130	135	
gta acc gaa atg ttg ggt aca ttt gct ctc tct gtt ggt gct gct gta				484
Val Thr Glu Met Leu Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val	140	145	150	155
gga atg gag ttt tgg gcg aga tgg gca cac aaa gca ctg tgg cat gct				532
Gly Met Glu Phe Trp Ala Arg Trp Ala His Lys Ala Leu Trp His Ala	160	165	170	
tca cta tgg cac atg cat gag tca cac cac aaa cca aga gaa gga cct				580
Ser Leu Trp His Met His Glu Ser His His Lys Pro Arg Glu Gly Pro	175	180	185	
ttt gag ctg aac gac gtt ttc gcc ata aca aac gct gtt cca gca ata				628
Phe Glu Leu Asn Asp Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile	190	195	200	
gcc ctc ctc aac tat ggt ttc ttc cat aaa ggc ctc att gcc gga cta				676
Ala Leu Leu Asn Tyr Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu	205	210	215	
tgc ttc ggt gct ggg cta ggg atc aca gta ttt gga atg gca tac atg				724
Cys Phe Gly Ala Gly Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met	220	225	230	235
ttt gtt cac gat ggt ttg gtt cac aag aga ttc cca gtt gga cct gta				772
Phe Val His Asp Gly Leu Val His Lys Arg Phe Pro Val Gly Pro Val	240	245	250	
gcc aat gta cct tat ctt agg aag gtg gct gct gct cat tcg ctt cat				820
Ala Asn Val Pro Tyr Leu Arg Lys Val Ala Ala Ala His Ser Leu His	255	260	265	
cac tca gag aag ttc aat ggt gtc cca tat ggc ttg ttc ttc gga cct				868
His Ser Glu Lys Phe Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro	270	275	280	
aag gaa ctg gaa gaa gta gga ggg acg gaa gag ttg gaa aag gaa gtg				916
Lys Glu Leu Glu Glu Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val	285	290	295	
ata cga agg acg aga ctt tcg aaa gga tca tgaacgattg ttcataaaca				966
Ile Arg Arg Thr Arg Leu Ser Lys Gly Ser				

300 305

tagaatgtca ttttacactt cttatcaatg aggaagggtg atttttgatg tatttgatag 1026

tagagaaaaa tgtagctctc ttgatgaaat gaatttgtat ttatgtaggc tcttcttatt 1086

cagtaagatt ttttcttttt tttgatctcg tgccgaatt 1125

<210> 110

<211> 309

<212> PRT

<213> Lycopersicon esculentum

<400> 110

Met Ala Ala Ala Ala Arg Ile Ser Ala Ser Ser Thr Ser Arg Thr Phe
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Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys Pro Thr Ser Thr Thr
 20 25 30

Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu Asn Leu Gly Pro Ile
 35 40 45

Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu
 50 55 60

Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu
65 70 75 80

Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg Leu Ala Glu Lys Leu
 85 90 95

Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu Val Ala Ala Ile Met
 100 105 110

Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met Ala Val Tyr Tyr Arg
 115 120 125

Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro Val Thr Glu Met Leu
 130 135 140

Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val Gly Met Glu Phe Trp
145 150 155 160

Ala Arg Trp Ala His Lys Ala Leu Trp His Ala Ser Leu Trp His Met

165

170

175

His Glu Ser His His Lys Pro Arg Glu Gly Pro Phe Glu Leu Asn Asp
 180 185 190

Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile Ala Leu Leu Asn Tyr
 195 200 205

Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu Cys Phe Gly Ala Gly
 210 215 220

Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met Phe Val His Asp Gly
 225 230 235 240

Leu Val His Lys Arg Phe Pro Val Gly Pro Val Ala Asn Val Pro Tyr
 245 250 255

Leu Arg Lys Val Ala Ala Ala His Ser Leu His His Ser Glu Lys Phe
 260 265 270

Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro Lys Glu Leu Glu Glu
 275 280 285

Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val Ile Arg Arg Thr Arg
 290 295 300

Leu Ser Lys Gly Ser
 305

<210> 111

<211> 1779

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<400> 111

atg gat ctc cgt cgg agg cct cct aaa cca ccg gtt acc aac aac aac 48
 Met Asp Leu Arg Arg Arg Pro Pro Lys Pro Pro Val Thr Asn Asn Asn
 1 5 10 15

aac tcc aac gga tct ttc cgt tct tat cag cct cgc act tcc gat gac 96
 Asn Ser Asn Gly Ser Phe Arg Ser Tyr Gln Pro Arg Thr Ser Asp Asp
 20 25 30

gat cat cgt cgc cgg gct aca aca att gct cct cca ccg aaa gca tcc	144
Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser	
35 40 45	
gac gcg ctt cct ctt ccg tta tat ctc aca aac gcc gtt ttc ttc acg	192
Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr	
50 55 60	
ctc ttc ttc tcc gtc gcg tat tac ctc ctc cac ccg tgg cgt gac aag	240
Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys	
65 70 75 80	
atc cgt tac aat acg cct ctt cac gtc gtc act atc aca gaa ctc ggc	288
Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly	
85 90 95	
gcc att att gct ctc atc gct tgc ttt atc tat ctc cta ggg ttt ttt	336
Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe	
100 105 110	
ggg att gac ttt gtt cag tca ttt atc tca cgt gcc tct ggt gat gct	384
Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala	
115 120 125	
tgg gat ctc gcc gat acg atc gat gat gat gac cac ccg ctt gtc acg	432
Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr	
130 135 140	
tgc tct cca ccg act ccg atc gtt tcc gtt gct aaa tta cct aat ccg	480
Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro	
145 150 155 160	
gaa cct att gtt acc gaa tgc ctt cct gag gaa gac gag gag att gtg	528
Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val	
165 170 175	
aaa tgc gtt atc gac gga gtt att cca tgc tac tgc ctt gaa tct cgt	576
Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg	
180 185 190	
ctc ggt gat tgc aaa aga gcg gcg tgc att cgt cgt gag gcg ttg cag	624
Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln	
195 200 205	
aga gtc acc ggg aga tgc att gaa ggg tta ccg ttg gat gga ttt gat	672
Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp	
210 215 220	
tat gaa tgc att ttg ggg caa tgc tgt gag atg cct gtt gga tac att	720
Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile	
225 230 235 240	
cag att cct gtt ggg att gct ggt cca ttg ttg ctt gat ggt tat gag	768
Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu	
245 250 255	
tac tct gtt cct atg gct aca acc gaa ggt tgt ttg gtt gct agc act	816
Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr	
260 265 270	

aac aga ggc tgc aag gct atg ttt atc tct ggt ggc gcc acc agt acc	864
Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr	
275 280 285	
gtt ctt aag gac ggt atg acc cga gca cct gtt gtt cgg ttc gct tcg	912
Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser	
290 295 300	
gcg aga cga gct tcg gag ctt aag ttt ttc ttg gag aat cca gag aac	960
Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn	
305 310 315 320	
ttt gat act ttg gca gta gtc ttc aac agg tcg agt aga ttt gca aga	1008
Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg	
325 330 335	
ctg caa agt gtt aaa tgc aca atc gcg ggg aag aat gct tat gta agg	1056
Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg	
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Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys	
355 360 365	
ggt gtg cag aat gtt ctt gag tat ctt acc gat gat ttc cct gac atg	1152
Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met	
370 375 380	
gat gtg att gga atc tct ggt aac ttc tgt tcg gac aag aaa cct gct	1200
Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala	
385 390 395 400	
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Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala	
405 410 415	
gta atc aga gga gag atc gtg aac aag gtc ttg aaa acg agc gtg gct	1296
Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala	
420 425 430	
gct tta gtc gag ctc aac atg ctc aag aac cta gct ggc tct gct gtt	1344
Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val	
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Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser	
450 455 460	
gct gta ttc ata gct act ggc caa gat cca gct caa aac gtg gag agt	1440
Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser	
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Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile	
485 490 495	
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His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly	
500 505 510	

gga aca cag ctt gca tct caa tca gcg tgt tta aac ctg ctc gga gtt 1584
 Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val
 515 520 525

aaa gga gca agc aca gag tcg ccg gga atg aac gca agg agg cta gcg 1632
 Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala
 530 535 540

acg atc gta gcc gga gca gtt tta gct gga gag tta tct tta atg tca 1680
 Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser
 545 550 555 560

gca att gca gct gga cag ctt gtg aga agt cac atg aaa tac aat aga 1728
 Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
 565 570 575

tcc agc cga gac atc tct gga gca acg aca acg aca aca aca aca aca 1776
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tga 1779

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 35 40 45

Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr
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Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys
 65 70 75 80

Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly
 85 90 95

Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe
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Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala
 115 120 125

Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr
 130 135 140

Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro
 145 150 155 160

Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val
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Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg
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Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln
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Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp
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Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile
 225 230 235 240

Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu
 245 250 255

Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr
 260 265 270

Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr
 275 280 285

Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser
 290 295 300

Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn
 305 310 315 320

Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg
 325 330 335

Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg
 340 345 350

Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys
 355 360 365

Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met
 370 375 380

Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala
 385 390 395 400

Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala
 405 410 415

Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala
 420 425 430

Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val
 435 440 445

Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser
 450 455 460

Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser
 465 470 475 480

Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile
 485 490 495

His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly
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Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val
 515 520 525

Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala
 530 535 540

Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser
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Phe Val Arg Glu Asn His Leu Ser Gly Ser Gly Ser Leu Arg Arg Arg	
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Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser	
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cca tcg gtg gtg atg gac tcc gat ttc gac gcc aag gtg ttc cgt aag	192
Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys	
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aac ttg acg aga agc gat aat tac aat cgt aaa ggg ttc ggt cat aag	240
Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys	
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gag gag aca ctc aag ctc atg aat cga gag tac acc agt gat ata ttg	288
Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu	
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gag aca ctg aaa aca aat ggg tat act tat tct tgg gga gat gtt act	336
Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr	
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gtg aaa ctc gct aaa gca tat ggt ttt tgc tgg ggt gtt gag cgt gct	384
Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala	
115 120 125	
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Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu	
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Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu	
145 150 155 160	
gaa gat atg gat gtt aaa att att ccg gtt gag gat tca aag aaa cag	528
Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln	
165 170 175	
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Val	Asp	Thr	Thr	Cys	Pro	Trp	Val	Thr	Lys	Val	Trp	Asn	Thr	Val	Glu		
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Thr	Gln	Glu	Arg	Gln	Asp	Ala	Ile	Tyr	Glu	Leu	Val	Glu	Glu	Lys	Ile		
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Asp	Leu	Met	Leu	Val	Val	Gly	Gly	Trp	Asn	Ser	Ser	Asn	Thr	Ser	His		
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ctt	cag	gaa	atc	tca	gag	gca	cgg	gga	atc	cca	tct	tac	tgg	atc	gat	1200	
Leu	Gln	Glu	Ile	Ser	Glu	Ala	Arg	Gly	Ile	Pro	Ser	Tyr	Trp	Ile	Asp		
385				390				395						400			
agt	gag	aaa	cgg	ata	gga	cct	ggg	aat	aaa	ata	gcc	tat	aag	ctc	cac	1248	
Ser	Glu	Lys	Arg	Ile	Gly	Pro	Gly	Asn	Lys	Ile	Ala	Tyr	Lys	Leu	His		
		405				410					415						
tat	gga	gaa	ctg	gtc	gag	aag	gaa	aac	ttt	ctc	cca	aag	gga	cca	ata	1296	

Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile
 420 425 430

aca atc ggt gtg aca tca ggt gca tca acc ccg gat aag gtc gtg gaa 1344
 Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu
 435 440 445

gat gct ttg gtg aag gtg ttc gac att aaa cgt gaa gag tta ttg cag 1392
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 35 40 45

Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys
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Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys
 65 70 75 80

Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu
 85 90 95

Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr
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Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala
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Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu
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Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu
145 150 155 160

Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln
165 170 175

Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly
180 185 190

Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile
195 200 205

Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu
210 215 220

Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn
225 230 235 240

His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile
245 250 255

Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly
260 265 270

Gly•Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys
275 280 285

Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val
290 295 300

Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu
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Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val
325 330 335

Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala
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Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile
355 360 365

Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His
370 375 380

Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp
385 390 395 400

Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His
405 410 415

Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile
420 425 430

Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu
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Val Val Ser Asp Ser Ser Lys Ala Thr Pro Leu Phe Ser Gly Trp Ile
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cat gga aca gat ctg cag ttt ttg ttc caa cac aag ctt act cat gag 144
His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu
35 40 45

gtc aag aaa agg tca cgt gtg gtt cag gct tcc tta tca gaa tct gga 192
Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
50 55 60

gaa tac tac aca cag aga ccg cca acg cct att ttg gac act gtg aac 240
Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
65 70 75 80

tat ccc att cat atg aaa aat ctg tct ctg aag gaa ctt aaa caa cta 288

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Ala	Asp	Glu	Leu	Arg	Ser	Asp	Thr	Ile	Phe	Asn	Val	Ser	Lys	Thr	Gly	
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Gly	His	Leu	Gly	Ser	Ser	Leu	Gly	Val	Val	Glu	Leu	Thr	Val	Ala	Leu	
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Glu	Ser	Glu	Tyr	Asp	Cys	Phe	Gly	Thr	Gly	His	Ser	Ser	Thr	Thr	Ile	
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Asn	Asn	Val	Ile	Ala	Val	Ile	Gly	Asp	Gly	Ala	Met	Thr	Ala	Gly	Gln	
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Asp	Gly	Pro	Val	Ala	Pro	Val	Gly	Ala	Leu	Ser	Ser	Ala	Leu	Ser	Arg	
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gat	gaa	tat	gct	cgt	ggc	atg	att	agt	ggc	tct	gga	tca	aca	ttg	ttt	960
Asp	Glu	Tyr	Ala	Arg	Gly	Met	Ile	Ser	Gly	Ser	Gly	Ser	Thr	Leu	Phe	
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Asp	Asp	Leu	Ile	Ala	Ile	Leu	Lys	Glu	Val	Arg	Ser	Thr	Lys	Thr	Thr		
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Tyr	Ala	Glu	Arg	Ala	Ala	Asp	Lys	Tyr	His	Gly	Val	Ala	Lys	Phe	Asp		
	370					375				380							
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Pro	Ala	Thr	Gly	Lys	Gln	Phe	Lys	Ala	Ser	Ala	Lys	Thr	Gln	Ser	Tyr		
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Thr	Thr	Tyr	Phe	Ala	Glu	Ala	Leu	Ile	Ala	Glu	Ala	Glu	Ala	Asp	Lys		
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gac	att	ggt	gca	atc	cat	gct	gcc	atg	ggg	ggt	ggg	acc	gga	atg	aac	1296	
Asp	Ile	Val	Ala	Ile	His	Ala	Ala	Met	Gly	Gly	Gly	Thr	Gly	Met	Asn		
		420					425						430				
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Leu	Phe	His	Arg	Arg	Phe	Pro	Thr	Arg	Cys	Phe	Asp	Val	Gly	Ile	Ala		
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gaa	caa	cat	gca	gta	acc	ttt	gct	gct	gga	ttg	gct	tgt	gaa	ggc	att	1392	
Glu	Gln	His	Ala	Val	Thr	Phe	Ala	Ala	Gly	Leu	Ala	Cys	Glu	Gly	Ile		
	450					455				460							
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Lys	Pro	Phe	Cys	Ala	Ile	Tyr	Ser	Ser	Phe	Met	Gln	Arg	Ala	Tyr	Asp		
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cag	gta	gtg	cat	gac	gtt	gat	ttg	caa	aag	ctg	ccc	gtg	agg	ttt	gca	1488	
Gln	Val	Val	His	Asp	Val	Asp	Leu	Gln	Lys	Leu	Pro	Val	Arg	Phe	Ala		
			485					490						495			
atg	gac	aga	gca	ggt	ctt	gtt	gga	gca	gat	ggt	cca	aca	cat	tgt	ggt	1536	
Met	Asp	Arg	Ala	Gly	Leu	Val	Gly	Ala	Asp	Gly	Pro	Thr	His	Cys	Gly		
		500					505						510				
gca	ttt	gat	gtt	act	tac	atg	gca	tgt	ctt	cct	aac	atg	gtt	gta	atg	1584	
Ala	Phe	Asp	Val	Thr	Tyr	Met	Ala	Cys	Leu	Pro	Asn	Met	Val	Val	Met		
		515					520					525					
gct	cct	tct	gat	gaa	gcg	gag	cta	ttt	cac	atg	gta	gca	act	gct	gcc	1632	
Ala	Pro	Ser	Asp	Glu	Ala	Glu	Leu	Phe	His	Met	Val	Ala	Thr	Ala	Ala		
	530					535					540						
gcc	att	gat	gac	aga	cca	agt	tgt	ttt	aga	tac	cca	aga	gga	aat	ggg	1680	
Ala	Ile	Asp	Asp	Arg	Pro	Ser	Cys	Phe	Arg	Tyr	Pro	Arg	Gly	Asn	Gly		
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Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val	
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ggt aaa ggt agg ata ttg att gag ggg gag aga gtg gct cta ttg gga	1776
Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly	
580 585 590	
tat ggc tca gca gtg cag aac tgt ttg gat gct gct att gtg cta gaa	1824
Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu	
595 600 605	
tcc cgc ggc tta caa gta aca gtt gca gat gca cgt ttc tgc aaa cca	1872
Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro	
610 615 620	
ctg gac cat gcc ctc ata agg agc ctt gca aaa tca cat gaa gtg cta	1920
Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu	
625 630 635 640	
atc act gtc gaa gaa gga tca att gga ggt ttt gga tct cat gtt gtt	1968
Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val	
645 650 655	
cag ttc atg gcc tta gat ggg ctt ctt gat ggc aag ttg aag tgg aga	2016
Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg	
660 665 670	
cca ata gtt ctt cct gat cga tac att gac cat gga tct cct gtt gat	2064
Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp	
675 680 685	
cag ttg gcg gaa gct ggc cta aca cca tct cac att gca gca aca gta	2112
Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val	
690 695 700	
ttt aac ata ctt gga caa acc aga gag gct cta gag gtc atg aca taa	2160
Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr	
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<211> 719

<212> PRT

<213> Lycopersicon esculentum

<400> 116

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35 40 45

Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
 50 55 60

Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
 65 70 75 80

Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu
 85 90 95

Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly
 100 105 110

Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu
 115 120 125

His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly
 130 135 140

His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met
 145 150 155 160

Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser
 165 170 175

Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile
 180 185 190

Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn
 195 200 205

Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln
 210 215 220

Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile
 225 230 235 240

Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu
 245 250 255

Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg
 260 265 270

Leu Gln Ser Asn Arg Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly
 275 280 285

Val Thr Lys Gln Ile Gly Gly Pro Met His Glu Leu Ala Ala Lys Val
 290 295 300

Asp Glu Tyr Ala Arg Gly Met Ile Ser Gly Ser Gly Ser Thr Leu Phe
 305 310 315 320

Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn Ile
 325 330 335

Asp Asp Leu Ile Ala Ile Leu Lys Glu Val Arg Ser Thr Lys Thr Thr
 340 345 350

Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr Pro
 355 360 365

Tyr Ala Glu Arg Ala Ala Asp Lys Tyr His Gly Val Ala Lys Phe Asp
 370 375 380

Pro Ala Thr Gly Lys Gln Phe Lys Ala Ser Ala Lys Thr Gln Ser Tyr
 385 390 395 400

Thr Thr Tyr Phe Ala Glu Ala Leu Ile Ala Glu Ala Glu Ala Asp Lys
 405 410 415

Asp Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Met Asn
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Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala
 435 440 445

Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile
 450 455 460

Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp
 465 470 475 480

Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala
 485 490 495

Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly
 500 505 510

Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met
 515 520 525

Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala
 530 535 540

Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly
 545 550 555 560

Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val
 565 570 575

Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly
 580 585 590

Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu
 595 600 605

Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro
 610 615 620

Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu
 625 630 635 640

Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val
 645 650 655

Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg
 660 665 670

Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp
 675 680 685

Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val
 690 695 700

Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr
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<210> 117

<211> 1434

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<400> 117

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ttc ttg gat acc tcc agg ttc aat cca atc cct aaa ctc tca ggt ggg	96
Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly	
20 25 30	
ttt agt ttg agg agg agg aat caa ggg aga ggt ttt gga aaa ggt gtt	144
Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val	
35 40 45	
aag tgt tca gtg aaa gtg cag cag caa caa caa cct cct cca gca tgg	192
Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp	
50 55 60	
cct ggg aga gct gtc cct gag gcg cct cgt caa tct tgg gat gga cca	240
Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro	
65 70 75 80	
aaa ccc atc tct atc gtt gga tct act ggt tct att ggc act cag aca	288
Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr	
85 90 95	
ttg gat att gtg gct gag aat cct gac aaa ttc aga gtt gtg gct cta	336
Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu	
100 105 110	
gct gct ggt tcg aat gtt act cta ctt gct gat cag gta agg aga ttt	384
Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe	
115 120 125	
aag cct gca ttg gtt gct gtt aga aac gag tca ctg att aat gag ctt	432
Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu	
130 135 140	
aaa gag gct tta gct gat ttg gac tat aaa ctc gag att att cca gga	480
Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly	
145 150 155 160	
gag caa gga gtg att gag gtt gcc cga cat cct gaa gct gta acc gtt	528
Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val	
165 170 175	
gtt acc gga ata gta ggt tgt gcg gga cta aag cct acg gtt gct gca	576
Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala	
180 185 190	
att gaa gca gga aag gac att gct ctt gca aac aaa gag aca tta atc	624
Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile	
195 200 205	
gca ggt ggt cct ttc gtg ctt ccg ctt gcc aac aaa cat aat gta aag	672
Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys	
210 215 220	
att ctt ccg gca gat tca gaa cat tct gcc ata ttt cag tgt att caa	720

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Gly	Leu	Pro	Glu	Gly	Ala	Leu	Arg	Lys	Ile	Ile	Leu	Thr	Ala	Ser	Gly	
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Gly	Ala	Phe	Arg	Asp	Trp	Pro	Val	Glu	Lys	Leu	Lys	Glu	Val	Lys	Val	
			260					265					270			
gcg	gat	gcg	ttg	aag	cat	cca	aac	tgg	aac	atg	gga	aag	aaa	atc	act	864
Ala	Asp	Ala	Leu	Lys	His	Pro	Asn	Trp	Asn	Met	Gly	Lys	Lys	Ile	Thr	
		275					280					285				
gtg	gac	tct	gct	acg	ctt	ttc	aac	aag	ggt	ctt	gag	gtc	att	gaa	gcg	912
Val	Asp	Ser	Ala	Thr	Leu	Phe	Asn	Lys	Gly	Leu	Glu	Val	Ile	Glu	Ala	
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cat	tat	ttg	ttt	gga	gct	gag	tat	gac	gat	ata	gag	att	gtc	att	cat	960
His	Tyr	Leu	Phe	Gly	Ala	Glu	Tyr	Asp	Asp	Ile	Glu	Ile	Val	Ile	His	
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ccg	caa	agt	atc	ata	cat	tcc	atg	att	gaa	aca	cag	gat	tca	tct	gtg	1008
Pro	Gln	Ser	Ile	Ile	His	Ser	Met	Ile	Glu	Thr	Gln	Asp	Ser	Ser	Val	
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ctt	gct	caa	ttg	ggt	tgg	cct	gat	atg	cgt	tta	ccg	att	ctc	tac	acc	1056
Leu	Ala	Gln	Leu	Gly	Trp	Pro	Asp	Met	Arg	Leu	Pro	Ile	Leu	Tyr	Thr	
		340					345					350				
atg	tca	tgg	ccc	gat	aga	ggt	cct	tgt	tct	gaa	gta	act	tgg	cca	aga	1104
Met	Ser	Trp	Pro	Asp	Arg	Val	Pro	Cys	Ser	Glu	Val	Thr	Trp	Pro	Arg	
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ctt	gac	ctt	tgc	aaa	ctc	ggt	tca	ttg	act	ttc	aag	aaa	cca	gac	aat	1152
Leu	Asp	Leu	Cys	Lys	Leu	Gly	Ser	Leu	Thr	Phe	Lys	Lys	Pro	Asp	Asn	
	370				375						380					
gtg	aaa	tac	cca	tcc	atg	gat	ctt	gct	tat	gct	gct	gga	cga	gct	gga	1200
Val	Lys	Tyr	Pro	Ser	Met	Asp	Leu	Ala	Tyr	Ala	Ala	Gly	Arg	Ala	Gly	
385				390				395						400		
ggc	aca	atg	act	gga	ggt	ctc	agc	gcc	gcc	aat	gag	aaa	gct	ggt	gaa	1248
Gly	Thr	Met	Thr	Gly	Val	Leu	Ser	Ala	Ala	Asn	Glu	Lys	Ala	Val	Glu	
			405					410					415			
atg	ttc	att	gat	gaa	aag	ata	agc	tat	ttg	gat	atc	ttc	aag	ggt	gtg	1296
Met	Phe	Ile	Asp	Glu	Lys	Ile	Ser	Tyr	Leu	Asp	Ile	Phe	Lys	Val	Val	
		420					425					430				
gaa	tta	aca	tgc	gat	aaa	cat	cga	aac	gag	ttg	gta	aca	tca	ccg	tct	1344
Glu	Leu	Thr	Cys	Asp	Lys	His	Arg	Asn	Glu	Leu	Val	Thr	Ser	Pro	Ser	
		435				440						445				
ctt	gaa	gag	att	ggt	cac	tat	gac	ttg	tgg	gca	cgt	gaa	tat	gcc	gcg	1392
Leu	Glu	Glu	Ile	Val	His	Tyr	Asp	Leu	Trp	Ala	Arg	Glu	Tyr	Ala	Ala	
	450				455					460						
aat	gtg	cag	ctt	tct	tct	ggt	gct	agg	cca	ggt	cat	gca	tga			1434

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<213> Arabidopsis thaliana

<400> 118.

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 20 25 30

Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val
 35 40 45

Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp
 50 55 60

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
 65 70 75 80

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
 85 90 95

Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu
 100 105 110

Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe
 115 120 125

Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu
 130 135 140

Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly
 145 150 155 160

Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
 165 170 175

Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
 180 185 190

Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
 195 200 205

Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
 210 215 220

Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
 225 230 235 240

Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
 245 250 255

Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
 260 265 270

Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
 275 280 285

Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
 290 295 300

His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
 305 310 315 320

Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
 325 330 335

Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
 340 345 350

Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
 355 360 365

Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
 370 375 380

Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
 385 390 395 400

Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
 405 410 415

Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
 420 425 430

Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
 435 440 445

Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
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<210> 119

<211> 884

<212> DNA

<213> Adonis palaestina clone ApIPI28

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cttccatcac taacagtcct cgccgagggt tgaatcggct gttcgcctca acgtcgact 179

atg ggt gaa gtc gct gat gct ggt atg gat gcc gtc cag aag cgg ctt 227
 Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu
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atg ttc gac gat gaa tgt att ttg gtg gat gag aat gac aag gtc gtc 275
 Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val
 20 25 30

gga cat gat tcc aaa tac aac tgt cat ttg atg gaa aag ata gag gca 323
 Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
 35 40 45

gaa aac ttg ctt cac aga gcc ttc agt gtt ttc tta ttc aac tca aaa 371
 Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60

tac gag ttg ctt ctt cag caa cga tct gca acg aag gta aca ttc ccg 419
 Tyr Glu Leu Leu Leu Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
 65 70 75 80

ctc gta tgg aca aac acc tgt tgc agc cat ccc ctc ttc cgt gat tcc 467
 Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
 85 90 95

gaa ctc ata gaa gaa aat ttt ctc ggg gta cga aac gct gca caa agg 515

Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110
 aag ctt tta gac gag cta ggc att cca gct gaa gac gta cca gtt gat 563
 Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
 115 120 125
 gaa ttc act cct ctt ggt cgc att ctt tac aaa gct cca tct gac gga 611
 Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140
 aaa tgg gga gag cac gaa ctg gac tat ctt ctg ttt att gtc cga gat 659
 Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 145 150 155 160
 gtg aaa tac gat cca aac cca gat gaa gtt gct gac gct aag tac gtt 707
 Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
 165 170 175
 aat cgc gag gag ttg aaa gag ata ctg aga aaa gct gat gca ggt gaa 755
 Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
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 gag gga ata aag ttg tct cct tgg ttt aga ttg gtt gtg gat aac ttt 803
 Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
 195 200 205
 ttg ttc aag tgg tgg gat cat gta gag gag ggg aag att aag gac gtc 851
 Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val
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 Ala Asp Met Lys Thr Ile His Lys Leu Thr
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<211> 234

<212> PRT

<213> Adonis palaestina clone ApIPI28

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 20 25 30

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
 35 40 45

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
65 70 75 80

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
85 90 95

Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
100 105 110

Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
115 120 125

Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
130 135 140

Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
145 150 155 160

Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
165 170 175

Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
180 185 190

Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
195 200 205

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210 215 220

Ala Asp Met Lys Thr Ile His Lys Leu Thr
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<211> 1402

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Phe Thr Arg Ser Val Ala Arg Ile Ser Ser Lys Phe Leu Arg Asn Arg
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agc ttc tat ggc tcc tct caa tct ctc gcc tct cat cgg ttc gca atc 153
Ser Phe Tyr Gly Ser Ser Gln Ser Leu Ala Ser His Arg Phe Ala Ile
20 25 30

att ccc gat cag ggt cac tct tgt tct gac tct cca cac aag ggt tac 201
Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys Gly Tyr
35 40 45 50

gtt tgc aga aca act tat tca ttg aaa tct ccg gtt ttt ggt gga ttt 249
Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly Gly Phe
55 60 65

agt cat caa ctc tat cac cag agt agc tcc ttg gtt gag gag gag ctt 297
Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu Glu Leu
70 75 80

gac cca ttt tcg ctt gtt gcc gat gag ctg tca ctt ctt agt aat aag 345
Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser Asn Lys
85 90 95

ttg aga gag atg gta ctt gcc gag gtt cca aag ctt gcc tct gct gct 393
Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser Ala Ala
100 105 110

gag tac ttc ttc aaa agg ggt gtg caa gga aaa cag ttt cgt tca act 441
Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg Ser Thr
115 120 125 130

att ttg ctg ctg atg gcg aca gct ctg gat gta cga gtt cca gaa gca 489
Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro Glu Ala
135 140 145

ttg att ggg gaa tca aca gat ata gtc aca tca gaa tta cgc gta agg 537
Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg
150 155 160

caa cgg ggt att gct gaa atc act gaa atg ata cac gtc gca agt cta 585
Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu
165 170 175

ctg cac gat gat gtc ttg gat gat gcc gat aca agg cgt ggt gtt ggt 633
Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly
180 185 190

tcc tta aat gtt gta atg ggt aac aag atg tcg gta tta gca gga gac 681
Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp
195 200 205 210

ttc ttg ctc tcc cgg gct tgt ggg gct ctc gct gct tta aag aac aca 729
Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr
215 220 225

gag gtt gta gca tta ctt gca act gct gta gaa cat ctt gtt acc ggt	777
Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly	
230 235 240	
gaa acc atg gag ata act agt tca acc gag cag cgt tat agt atg gac	825
Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp	
245 250 255	
tac tac atg cag aag aca tat tat aag aca gca tcg cta atc tct aac	873
Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn	
260 265 270	
agc tgc aaa gct gtt gcc gtt ctc act gga caa aca gca gaa gtt gcc	921
Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala	
275 280 285 290	
gtg tta gct ttt gag tat ggg agg aat ctg ggt tta gca ttc caa tta	969
Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu	
295 300 305	
ata gac gac att ctt gat ttc acg ggc aca tct gcc tct ctc gga aag	1017
Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys	
310 315 320	
gga tcg ttg tca gat att cgc cat gga gtc ata aca gcc cca atc ctc	1065
Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu	
325 330 335	
ttt gcc atg gaa gag ttt cct caa cta cgc gaa gtt gtt gat caa gtt	1113
Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val	
340 345 350	
gaa aaa gat cct agg aat gtt gac att gct tta gag tat ctt ggg aag	1161
Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys	
355 360 365 370	
agc aag gga ata cag agg gca aga gaa tta gcc atg gaa cat gcg aat	1209
Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn	
375 380 385	
cta gca gca gct gca atc ggg tct cta cct gaa aca gac aat gaa gat	1257
Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn Glu Asp	
390 395 400	
gtc aaa aga tcg agg cgg gca ctt att gac ttg acc cat aga gtc atc	1305
Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg Val Ile	
405 410 415	
acc aga aac aag tgagattaag taatgtttct ctctatacac caaaacattc	1357
Thr Arg Asn Lys	
420	
ctcatttcat ttgtaggatt ttgttggtcc aattcgtttc acgaa	1402

<210> 122

<211> 422

<212> PRT

<213> Arabidopsis thaliana

<400> 122

Met Leu Phe Thr Arg Ser Val Ala Arg Ile Ser Ser Lys Phe Leu Arg
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Asn Arg Ser Phe Tyr Gly Ser Ser Gln Ser Leu Ala Ser His Arg Phe
 20 25 30

Ala Ile Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys
 35 40 45

Gly Tyr Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly
 50 55 60

Gly Phe Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu
 65 70 75 80

Glu Leu Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser
 85 90 95

Asn Lys Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser
 100 105 110

Ala Ala Glu Tyr Phe Phe Lys Arg Gly Val Glu Gly Lys Gln Phe Arg
 115 120 125

Ser Thr Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro
 130 135 140

Glu Ala Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg
 145 150 155 160

Val Arg Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala
 165 170 175

Ser Leu Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly
 180 185 190

Val Gly Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala
 195 200 205

Gly Asp Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys
 210 215 220

Asn Thr Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val
 225 230 235 240

Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser
 245 250 255

Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile
 260 265 270

Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu
 275 280 285

Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe
 290 295 300

Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu
 305 310 315 320

Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro
 325 330 335

Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp
 340 345 350

Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu
 355 360 365

Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His
 370 375 380

Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn
 385 390 395 400

Glu Asp Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg
 405 410 415

Val Ile Thr Arg Asn Lys
 420

<210> 123

<211> 1155

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<400> 123

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Met Ser Val Ser Cys Cys Cys Arg Asn Leu Gly Lys Thr Ile Lys Lys	
1 5 10 15	
gca ata cct tca cat cat ttg cat ctg aga agt ctt ggt ggg agt ctc	96
Ala Ile Pro Ser His His Leu His Leu Arg Ser Leu Gly Gly Ser Leu	
20 25 30	
tat cgt cgt cgt atc caa agc tct tca atg gag acc gat ctc aag tca	144
Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser	
35 40 45	
acc ttt ctc aac gtt tat tct gtt ctc aag tct gac ctt ctt cat gac	192
Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp	
50 55 60	
cct tcc ttc gaa ttc acc aat gaa tct cgt ctc tgg gtt gat cgg atg	240
Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met	
65 70 75 80	
ctg gac tac aat gta cgt gga ggg aaa ctc aat cgg ggt ctc tct gtt	288
Leu Asp Tyr Asn Val Arg Gly Gly Lys Leu Asn Arg Gly Leu Ser Val	
85 90 95	
gtt gac agt ttc aaa ctt ttg aag caa ggc aat gat ttg act gag caa	336
Val Asp Ser Phe Lys Leu Leu Lys Gln Gly Asn Asp Leu Thr Glu Gln	
100 105 110	
gag gtt ttc ctc tct tgt gct ctc ggt tgg tgc att gaa tgg ctc caa	384
Glu Val Phe Leu Ser Cys Ala Leu Gly Trp Cys Ile Glu Trp Leu Gln	
115 120 125	
gct tat ttc ctt gtg ctt gat gat att atg gat aac tct gtc act cgc	432
Ala Tyr Phe Leu Val Leu Asp Asp Ile Met Asp Asn Ser Val Thr Arg	
130 135 140	
cgt ggt caa cct tgc tgg ttc aga gtt cct cag gtt ggt atg gtt gcc	480
Arg Gly Gln Pro Cys Trp Phe Arg Val Pro Gln Val Gly Met Val Ala	
145 150 155 160	
atc aat gat ggg att cta ctt cgc aat cac atc cac agg att ctc aaa	528
Ile Asn Asp Gly Ile Leu Leu Arg Asn His Ile His Arg Ile Leu Lys	
165 170 175	
aag cat ttc cgt gat aag cct tac tat gtt gac ctt gtt gat ttg ttt	576
Lys His Phe Arg Asp Lys Pro Tyr Tyr Val Asp Leu Val Asp Leu Phe	
180 185 190	
aat gag gtt gag ttg caa aca gct tgt ggc cag atg ata gat ttg atc	624
Asn Glu Val Glu Leu Gln Thr Ala Cys Gly Gln Met Ile Asp Leu Ile	
195 200 205	
acc acc ttt gaa gga gaa aag gat ttg gcc aag tac tca ttg tca atc	672

Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile		
210						215					220						
cac	cgt	cgt	att	gtc	cag	tac	aaa	acg	gct	tat	tac	tca	ttt	tat	ctc	720	
His	Arg	Arg	Ile	Val	Gln	Tyr	Lys	Thr	Ala	Tyr	Tyr	Ser	Phe	Tyr	Leu		
225					230					235					240		
cct	ggt	gct	tgt	gcg	ttg	ctt	atg	gcg	ggc	gaa	aat	ttg	gaa	aac	cat	768	
Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His		
				245					250					255			
att	gac	gtg	aaa	aat	ggt	ctt	ggt	gac	atg	gga	atc	tac	ttc	caa	gtg	816	
Ile	Asp	Val	Lys	Asn	Val	Leu	Val	Asp	Met	Gly	Ile	Tyr	Phe	Gln	Val		
			260						265					270			
cag	gat	gat	tat	ctg	gat	tgt	ttt	gct	gat	ccc	gag	acg	ctt	ggc	aag	864	
Gln	Asp	Asp	Tyr	Leu	Asp	Cys	Phe	Ala	Asp	Pro	Glu	Thr	Leu	Gly	Lys		
			275				280					285					
ata	gga	aca	gat	ata	gaa	gat	ttc	aaa	tgc	tcg	tgg	ttg	gtg	ggt	aag	912	
Ile	Gly	Thr	Asp	Ile	Glu	Asp	Phe	Lys	Cys	Ser	Trp	Leu	Val	Val	Lys		
	290					295					300						
gca	tta	gag	cgc	tgc	agc	gaa	gaa	caa	act	aag	ata	tta	tat	gag	aac	960	
Ala	Leu	Glu	Arg	Cys	Ser	Glu	Glu	Gln	Thr	Lys	Ile	Leu	Tyr	Glu	Asn		
305				310					315					320			
tat	ggt	aaa	ccc	gac	cca	tcg	aac	ggt	gct	aaa	gtg	aag	gat	ctc	tac	1008	
Tyr	Gly	Lys	Pro	Asp	Pro	Ser	Asn	Val	Ala	Lys	Val	Lys	Asp	Leu	Tyr		
				325					330					335			
aaa	gag	ctg	gat	ctt	gag	gga	ggt	ttc	atg	gag	tat	gag	agc	aaa	agc	1056	
Lys	Glu	Leu	Asp	Leu	Glu	Gly	Val	Phe	Met	Glu	Tyr	Glu	Ser	Lys	Ser		
			340					345					350				
tac	gag	aag	ctg	act	gga	gcg	att	gag	gga	cac	caa	agt	aaa	gca	atc	1104	
Tyr	Glu	Lys	Leu	Thr	Gly	Ala	Ile	Glu	Gly	His	Gln	Ser	Lys	Ala	Ile		
		355				360						365					
caa	gca	gtg	cta	aaa	tcc	ttc	ttg	gct	aag	atc	tac	aag	agg	cag	aag	1152	
Gln	Ala	Val	Leu	Lys	Ser	Phe	Leu	Ala	Lys	Ile	Tyr	Lys	Arg	Gln	Lys		
	370					375				380							
tag																1155	

<210> 124

<211> 384

<212> PRT

<213> Arabidopsis thaliana

<400> 124

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Ala Ile Pro Ser His His Leu His Leu Arg Ser Leu Gly Gly Ser Leu
20 25 30

Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser
35 40 45

Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp
50 55 60

Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met
65 70 75 80

Leu Asp Tyr Asn Val Arg Gly Gly Lys Leu Asn Arg Gly Leu Ser Val
85 90 95

Val Asp Ser Phe Lys Leu Leu Lys Gln Gly Asn Asp Leu Thr Glu Gln
100 105 110

Glu Val Phe Leu Ser Cys Ala Leu Gly Trp Cys Ile Glu Trp Leu Gln
115 120 125

Ala Tyr Phe Leu Val Leu Asp Asp Ile Met Asp Asn Ser Val Thr Arg
130 135 140

Arg Gly Gln Pro Cys Trp Phe Arg Val Pro Gln Val Gly Met Val Ala
145 150 155 160

Ile Asn Asp Gly Ile Leu Leu Arg Asn His Ile His Arg Ile Leu Lys
165 170 175

Lys His Phe Arg Asp Lys Pro Tyr Tyr Val Asp Leu Val Asp Leu Phe
180 185 190

Asn Glu Val Glu Leu Gln Thr Ala Cys Gly Gln Met Ile Asp Leu Ile
195 200 205

Thr Thr Phe Glu Gly Glu Lys Asp Leu Ala Lys Tyr Ser Leu Ser Ile
210 215 220

His Arg Arg Ile Val Gln Tyr Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu
225 230 235 240

Pro Val Ala Cys Ala Leu Leu Met Ala Gly Glu Asn Leu Glu Asn His
245 250 255

Ile Asp Val Lys Asn Val Leu Val Asp Met Gly Ile Tyr Phe Gln Val
 260 265 270

Gln Asp Asp Tyr Leu Asp Cys Phe Ala Asp Pro Glu Thr Leu Gly Lys
 275 280 285

Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys
 290 295 300

Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn
 305 310 315 320

Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr
 325 330 335

Lys Glu Leu Asp Leu Glu Gly Val Phe Met Glu Tyr Glu Ser Lys Ser
 340 345 350

Tyr Glu Lys Leu Thr Gly Ala Ile Glu Gly His Gln Ser Lys Ala Ile
 355 360 365

Gln Ala Val Leu Lys Ser Phe Leu Ala Lys Ile Tyr Lys Arg Gln Lys
 370 375 380

<210> 125

<211> 1101

<212> DNA

<213> Sinabs alba

<220>

<221> CDS

<400> 125

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 1 5 10 15

cat cct tca act atc tta acc caa tcc aga tcc aga tct cct cct tct 96
 His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser
 20 25 30

ctc atc acc ctt aaa ccc atc tcc ctc act cca aaa cgc acc gtt tcg 144
 Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser
 35 40 45

tct tct tcc tcc tct tcc ctc atc acc aaa gaa gac aac aac ctc aaa 192
 Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys
 50 55 60

tcc tct tcc tct tcc ttc gat ttc atg tct tac atc atc cgc aaa gcc	240
Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala	
65 70 75 80	
gac tcc gtc aac aaa gcc tta gac tcc gcc gtc cct ctc cgg gag cca	288
Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro	
85 90 95	
ctc aag atc cac gaa gcg atg cgt tac tct ctc ctc gcc gga gga aaa	336
Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys	
100 105 110	
cgc gtc aga cca gtt ctc tgc atc gcc gcg tgc gag cta gtc gga gga	384
Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly	
115 120 125	
gaa gag tct tta gct atg ccg gcg cgt tgc gcc gtg gaa atg atc cac	432
Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His	
130 135 140	
acc atg tcg ttg atc cac gac gac ttg cct tgt atg gat aac gac gat	480
Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp	
145 150 155 160	
ctc cgc cgc gga aag ccc acg aat cac aaa gtt tac ggc gaa gac gtg	528
Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val	
165 170 175	
gcg gtt tta gcc gga gac gcg ctt ctt tcg ttc gcc ttc gag cat tta	576
Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu	
180 185 190	
gcg tcg gct acg agc tcg gag gtt tct ccg gcg aga gtg gtt aga gct	624
Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala	
195 200 205	
gtg gga gag ttg gct aaa gcc atc ggc acc gaa ggg ctc gtg gcg gga	672
Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly	
210 215 220	
caa gtg gtg gat ata agc agt gaa ggg ttg gac tta aac aac gtc gga	720
Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly	
225 230 235 240	
ttg gag cat ttg aag ttt ata cat ttg cat aaa acg gcg gcg ttg ctt	768
Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu	
245 250 255	
gaa gct tca gcg gtt ttg ggt ggg atc atc ggt gga ggg agt gat gaa	816
Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu	
260 265 270	
gag atc gag agg ctg agg aag ttc gcg agg tgt att ggg ttg ttg ttt	864
Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys Ile Gly Leu Leu Phe	
275 280 285	
cag gtg gtt gat gat atc ttg gac gtg acg aaa tcg tct caa gaa ctg	912
Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu	
290 295 300	

ggg aaa acc gct ggg aaa gat ttg att gct gat aag ttg act tat ccg 960
 Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro
 305 310 315 320

aag ctc atg ggt ttg gag aaa tcg aga gag ttc gct gag aag ttg aat 1008
 Lys Leu Met Gly Leu Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn
 325 330 335

aca gag gca cgt gat cag ctt tta ggg ttt gat tcc gac aag gtt gct 1056
 Thr Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp Ser Asp Lys Val Ala
 340 345 350

cct ttg ttg gct ttg gct aat tac att gcc aat aga cag aac tga 1101
 Pro Leu Leu Ala Leu Ala Asn Tyr Ile Ala Asn Arg Gln Asn
 355 360 365

<210> 126

<211> 366

<212> PRT

<213> Sinabs alba

<400> 126

Met Ala Ser Ser Val Thr Pro Leu Gly Ser Trp Val Leu Leu His His
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His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser
 20 25 30

Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser
 35 40 45

Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys
 50 55 60

Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala
 65 70 75 80

Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro
 85 90 95

Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
 100 105 110

Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly
 115 120 125

Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His
 130 135 140

Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp
 145 150 155 160

Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val
 165 170 175

Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu
 180 185 190

Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala
 195 200 205

Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly
 210 215 220

Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly
 225 230 235 240

Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu
 245 250 255

Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu
 260 265 270

Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys Ile Gly Leu Leu Phe
 275 280 285

Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu
 290 295 300

Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro
 305 310 315 320

Lys Leu Met Gly Leu Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn
 325 330 335

Thr Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp Ser Asp Lys Val Ala
 340 345 350

Pro Leu Leu Ala Leu Ala Asn Tyr Ile Ala Asn Arg Gln Asn
 355 360 365

<210> 127

<211> 930

<212> DNA

<213> Erwinia uredovora

<220>

<221> CDS

<400> 127

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Met Asn Asn Pro Ser Leu Leu Asn His Ala Val Glu Thr Met Ala Val	
1 5 10 15	
ggc tcg aaa agt ttt gcg aca gcc tca aag tta ttt gat gca aaa acc	96
Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr	
20 25 30	
cgg cgc agc gta ctg atg ctc tac gcc tgg tgc cgc cat tgt gac gat	144
Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp	
35 40 45	
gtt att gac gat cag acg ctg ggc ttt cag gcc cgg cag cct gcc tta	192
Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu	
50 55 60	
caa acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag	240
Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln	
65 70 75 80	
gcc tat gca gga tcg cag atg cac gaa ccg gcg ttt gcg gct ttt cag	288
Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln	
85 90 95	
gaa gtg gct atg gct cat gat atc gcc ccg gct tac gcg ttt gat cat	336
Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His	
100 105 110	
ctg gaa ggc ttc gcc atg gat gta cgc gaa gcg caa tac agc caa ctg	384
Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu	
115 120 125	
gat gat acg ctg cgc tat tgc tat cac gtt gca ggc gtt gtc ggc ttg	432
Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu	
130 135 140	
atg atg gcg caa atc atg ggc gtg cgg gat aac gcc acg ctg gac cgc	480
Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg	
145 150 155 160	
gcc tgt gac ctt ggg ctg gca ttt cag ttg acc aat att gct cgc gat	528
Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp	
165 170 175	
att gtg gac gat gcg cat gcg ggc cgc tgt tat ctg ccg gca agc tgg	576
Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp	
180 185 190	

ctg gag cat gaa ggt ctg aac aaa gag aat tat gcg gca cct gaa aac 624
 Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn
 195 200 205

 cgt cag gcg ctg agc cgt atc gcc cgt cgt ttg gtg cag gaa gca gaa 672
 Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu
 210 215 220

 cct tac tat ttg tct gcc aca gcc ggc ctg gca ggg ttg ccc ctg cgt 720
 Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg
 225 230 235 240

 tcc gcc tgg gca atc gct acg gcg aag cag gtt tac cgg aaa ata ggt 768
 Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly
 245 250 255

 gtc aaa gtt gaa cag gcc ggt cag caa gcc tgg gat cag cgg cag tca 816
 Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser
 260 265 270

 acg acc acg ccc gaa aaa tta acg ctg ctg ctg gcc gcc tct ggt cag 864
 Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
 275 280 285

 gcc ctt act tcc cgg atg cgg gct cat cct ccc cgc cct gcg cat ctc 912
 Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu
 290 295 300

 tgg cag cgc ccg ctc tag 930
 Trp Gln Arg Pro Leu
 305

<210> 128

<211> 309

<212> PRT

<213> Erwinia uredovora

<400> 128

Met Asn Asn Pro Ser Leu Leu Asn His Ala Val Glu Thr Met Ala Val
 1 5 10 15

Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr
 20 25 30

Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp
 35 40 45

Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu
 50 55 60

Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln
65 70 75 80

Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln
85 90 95

Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His
100 105 110

Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu
115 120 125

Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu
130 135 140

Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg
145 150 155 160

Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp
165 170 175

Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp
180 185 190

Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn
195 200 205

Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu
210 215 220

Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg
225 230 235 240

Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly
245 250 255

Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser
260 265 270

Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
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Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu
290 295 300

Trp Gln Arg Pro Leu
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<211> 1479

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<213> *Erwinia uredovora*

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gca att cgt cta caa gct gcg ggg atc ccc gtc tta ctg ctt gaa caa	96
Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln	
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cgt gat aaa ccc ggc ggt cgg gct tat gtc tac gag gat cag ggg ttt	144
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe	
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acc ttt gat gca ggc ccg acg gtt atc acc gat ccc agt gcc att gaa	192
Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu	
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gaa ctg ttt gca ctg gca gga aaa cag tta aaa gag tat gtc gaa ctg	240
Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu	
65 70 75 80	
ctg ccg gtt acg ccg ttt tac cgc ctg tgt tgg gag tca ggg aag gtc	288
Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val	
85 90 95	
ttt aat tac gat aac gat caa acc cgg ctc gaa gcg cag att cag cag	336
Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln	
100 105 110	
ttt aat ccc cgc gat gtc gaa ggt tat cgt cag ttt ctg gac tat tca	384
Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser	
115 120 125	
cgc gcg gtg ttt aaa gaa ggc tat cta aag ctc ggt act gtc cct ttt	432
Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe	
130 135 140	
tta tcg ttc aga gac atg ctt cgc gcc gca cct caa ctg gcg aaa ctg	480
Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu	
145 150 155 160	
cag gca tgg aga agc gtt tac agt aag gtt gcc agt tac atc gaa gat	528

Gln	Ala	Trp	Arg	Ser	Val	Tyr	Ser	Lys	Val	Ala	Ser	Tyr	Ile	Glu	Asp	
				165					170					175		
gaa	cat	ctg	cgc	cag	gcg	ttt	tct	ttc	cac	tcg	ctg	ttg	gtg	ggc	ggc	576
Glu	His	Leu	Arg	Gln	Ala	Phe	Ser	Phe	His	Ser	Leu	Leu	Val	Gly	Gly	
			180					185					190			
aat	ccc	ttc	gcc	acc	tca	tcc	att	tat	acg	ttg	ata	cac	gcg	ctg	gag	624
Asn	Pro	Phe	Ala	Thr	Ser	Ser	Ile	Tyr	Thr	Leu	Ile	His	Ala	Leu	Glu	
		195					200					205				
cgt	gag	tgg	ggc	gtc	tgg	ttt	ccg	cgt	ggc	ggc	acc	ggc	gca	tta	gtt	672
Arg	Glu	Trp	Gly	Val	Trp	Phe	Pro	Arg	Gly	Gly	Thr	Gly	Ala	Leu	Val	
	210					215					220					
cag	ggg	atg	ata	aag	ctg	ttt	cag	gat	ctg	ggt	ggc	gaa	gtc	gtg	tta	720
Gln	Gly	Met	Ile	Lys	Leu	Phe	Gln	Asp	Leu	Gly	Gly	Glu	Val	Val	Leu	
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aac	gcc	aga	gtc	agc	cat	atg	gaa	acg	aca	gga	aac	aag	att	gaa	gcc	768
Asn	Ala	Arg	Val	Ser	His	Met	Glu	Thr	Thr	Gly	Asn	Lys	Ile	Glu	Ala	
			245						250					255		
gtg	cat	tta	gag	gac	ggc	cgc	agg	ttc	ctg	acg	caa	gcc	gtc	gcg	tca	816
Val	His	Leu	Glu	Asp	Gly	Arg	Arg	Phe	Leu	Thr	Gln	Ala	Val	Ala	Ser	
		260						265					270			
aat	gca	gat	gtg	gtt	cat	acc	tat	cgc	gac	ctg	tta	agc	cag	cac	cct	864
Asn	Ala	Asp	Val	Val	His	Thr	Tyr	Arg	Asp	Leu	Leu	Ser	Gln	His	Pro	
		275					280					285				
gcc	gcg	gtt	aag	cag	tcc	aac	aaa	ctg	cag	act	aag	cgc	atg	agt	aac	912
Ala	Ala	Val	Lys	Gln	Ser	Asn	Lys	Leu	Gln	Thr	Lys	Arg	Met	Ser	Asn	
	290					295					300					
tct	ctg	ttt	gtg	ctc	tat	ttt	ggt	ttg	aat	cac	cat	cat	gat	cag	ctc	960
Ser	Leu	Phe	Val	Leu	Tyr	Phe	Gly	Leu	Asn	His	His	His	Asp	Gln	Leu	
305					310					315					320	
gcg	cat	cac	acg	gtt	tgt	ttc	ggc	ccg	cgt	tac	cgc	gag	ctg	att	gac	1008
Ala	His	His	Thr	Val	Cys	Phe	Gly	Pro	Arg	Tyr	Arg	Glu	Leu	Ile	Asp	
			325					330					335			
gaa	att	ttt	aat	cat	gat	ggc	ctc	gca	gag	gac	ttc	tca	ctt	tat	ctg	1056
Glu	Ile	Phe	Asn	His	Asp	Gly	Leu	Ala	Glu	Asp	Phe	Ser	Leu	Tyr	Leu	
		340						345					350			
cac	gcg	ccc	tgt	gtc	acg	gat	tcg	tca	ctg	gcg	cct	gaa	ggt	tgc	ggc	1104
His	Ala	Pro	Cys	Val	Thr	Asp	Ser	Ser	Leu	Ala	Pro	Glu	Gly	Cys	Gly	
		355					360					365				
agt	tac	tat	gtg	ttg	gcg	ccg	gtg	ccg	cat	tta	ggc	acc	gcg	aac	ctc	1152
Ser	Tyr	Tyr	Val	Leu	Ala	Pro	Val	Pro	His	Leu	Gly	Thr	Ala	Asn	Leu	
	370					375					380					
gac	tgg	acg	gtt	gag	ggg	cca	aaa	cta	cgc	gac	cgt	att	ttt	gcg	tac	1200
Asp	Trp	Thr	Val	Glu	Gly	Pro	Lys	Leu	Arg	Asp	Arg	Ile	Phe	Ala	Tyr	
	385				390					395					400	
ctt	gag	cag	cat	tac	atg	cct	ggc	tta	cgg	agt	cag	ctg	gtc	acg	cac	1248

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415
 cgg atg ttt acg ccg ttt gat ttt cgc gac cag ctt aat gcc tat cat 1296
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430
 ggc tca gcc ttt tct gtg gag ccc gtt ctt acc cag agc gcc tgg ttt 1344
 Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445
 cgg ccg cat aac cgc gat aaa acc att act aat ctc tac ctg gtc ggc 1392
 Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
 450 455 460
 gca ggc acg cat ccc ggc gca ggc att cct ggc gtc atc ggc tcg gca 1440
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480
 aaa gcg aca gca ggt ttg atg ctg gag gat ctg ata tga 1479
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
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 35 40 45
 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60
 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu
 65 70 75 80
 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95
 Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln
 100 105 110

Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser
 115 120 125

Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
 130 135 140

Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
 145 150 155 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp
 165 170 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
 180 185 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
 195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
 210 215 220

Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
 225 230 235 240

Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala
 245 250 255

Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser
 260 265 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
 275 280 285

Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn
 290 295 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
 305 310 315 320

Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp
 325 330 335

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
 340 345 350

His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly
 355 360 365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
 370 375 380

Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr
 385 390 395 400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430

Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445

Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
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Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
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<211> 1725

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<213> Narcissus pseudonarcissus

<220>

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 1 5 10 15

gga aag aaa gtg aag atg aac acg atg att cga tcg aag ttg ttt tca 96
 Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser
 20 25 30

att cgg tcg gct ttg gac act aag gtg tct gat atg agc gtc aat gct 144

Ile	Arg	Ser	Ala	Leu	Asp	Thr	Lys	Val	Ser	Asp	Met	Ser	Val	Asn	Ala		
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cca	aaa	gga	ttg	ttt	cca	cca	gag	cct	gag	cac	tac	agg	ggg	cca	aag	192	
Pro	Lys	Gly	Leu	Phe	Pro	Pro	Glu	Pro	Glu	His	Tyr	Arg	Gly	Pro	Lys		
	50						55				60						
ctt	aaa	gtg	gct	atc	att	gga	gct	ggg	ctc	gct	ggc	atg	tca	act	gca	240	
Leu	Lys	Val	Ala	Ile	Ile	Gly	Ala	Gly	Leu	Ala	Gly	Met	Ser	Thr	Ala		
	65					70				75					80		
gtg	gag	ctt	ttg	gat	caa	ggg	cat	gag	gtt	gac	ata	tat	gaa	tcc	aga	288	
Val	Glu	Leu	Leu	Asp	Gln	Gly	His	Glu	Val	Asp	Ile	Tyr	Glu	Ser	Arg		
				85					90					95			
caa	ttt	att	ggt	ggt	aaa	gtc	ggt	tct	ttt	gta	gat	aag	cgt	gga	aac	336	
Gln	Phe	Ile	Gly	Gly	Lys	Val	Gly	Ser	Phe	Val	Asp	Lys	Arg	Gly	Asn		
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cat	att	gaa	atg	gga	ctc	cat	gtg	ttt	ttt	ggt	tgc	tat	aac	aat	ctt	384	
His	Ile	Glu	Met	Gly	Leu	His	Val	Phe	Phe	Gly	Cys	Tyr	Asn	Asn	Leu		
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ttc	aga	ctt	atg	aaa	aag	gta	ggt	gca	gat	gaa	aat	tta	ctg	gtg	aag	432	
Phe	Arg	Leu	Met	Lys	Lys	Val	Gly	Ala	Asp	Glu	Asn	Leu	Leu	Val	Lys		
	130					135					140						
gat	cat	act	cat	acc	ttt	gta	aac	cga	ggt	gga	gaa	att	ggt	gaa	ctt	480	
Asp	His	Thr	His	Thr	Phe	Val	Asn	Arg	Gly	Gly	Glu	Ile	Gly	Glu	Leu		
	145				150					155					160		
gat	ttc	cga	ctt	ccg	atg	ggt	gca	cca	tta	cat	ggt	att	cgt	gca	ttt	528	
Asp	Phe	Arg	Leu	Pro	Met	Gly	Ala	Pro	Leu	His	Gly	Ile	Arg	Ala	Phe		
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cta	aca	act	aat	caa	ctg	aag	cct	tat	gat	aaa	gca	agg	aat	gct	gtg	576	
Leu	Thr	Thr	Asn	Gln	Leu	Lys	Pro	Tyr	Asp	Lys	Ala	Arg	Asn	Ala	Val		
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gct	ctt	gcc	ctt	agc	cca	gtt	gta	cgt	gct	ctt	att	gat	cca	aat	ggt	624	
Ala	Leu	Ala	Leu	Ser	Pro	Val	Val	Arg	Ala	Leu	Ile	Asp	Pro	Asn	Gly		
	195					200						205					
gca	atg	cag	gat	ata	agg	aac	tta	gat	aat	att	agc	ttt	tct	gat	tgg	672	
Ala	Met	Gln	Asp	Ile	Arg	Asn	Leu	Asp	Asn	Ile	Ser	Phe	Ser	Asp	Trp		
	210					215					220						
ttc	tta	tcc	aaa	ggc	ggt	acc	cgc	atg	agc	atc	caa	agg	atg	tgg	gat	720	
Phe	Leu	Ser	Lys	Gly	Gly	Thr	Arg	Met	Ser	Ile	Gln	Arg	Met	Trp	Asp		
	225				230					235					240		
cca	gtt	gct	tat	gcc	ctc	gga	ttt	att	gac	tgt	gat	aat	atc	agt	gcc	768	
Pro	Val	Ala	Tyr	Ala	Leu	Gly	Phe	Ile	Asp	Cys	Asp	Asn	Ile	Ser	Ala		
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cgt	tgt	atg	ctt	act	ata	ttt	tct	cta	ttt	gct	act	aag	aca	gaa	gct	816	
Arg	Cys	Met	Leu	Thr	Ile	Phe	Ser	Leu	Phe	Ala	Thr	Lys	Thr	Glu	Ala		
			260					265					270				
tct	ctg	ttg	cgt	atg	ttg	aag	ggt	tcg	cct	gat	gtt	tac	tta	agc	ggt	864	

Ser	Leu	Leu	Arg	Met	Leu	Lys	Gly	Ser	Pro	Asp	Val	Tyr	Leu	Ser	Gly	
	275						280					285				
cct	ata	aga	aag	tat	att	aca	gat	aaa	ggg	gga	agg	ttt	cac	cta	agg	912
Pro	Ile	Arg	Lys	Tyr	Ile	Thr	Asp	Lys	Gly	Gly	Arg	Phe	His	Leu	Arg	
	290					295					300					
tgg	ggg	tgt	aga	gag	ata	ctt	tat	gat	gaa	cta	tca	aat	ggc	gac	aca	960
Trp	Gly	Cys	Arg	Glu	Ile	Leu	Tyr	Asp	Glu	Leu	Ser	Asn	Gly	Asp	Thr	
305					310					315					320	
tat	atc	aca	ggc	att	gca	atg	tcg	aag	gct	acc	aat	aaa	aaa	ctt	gtg	1008
Tyr	Ile	Thr	Gly	Ile	Ala	Met	Ser	Lys	Ala	Thr	Asn	Lys	Lys	Leu	Val	
			325					330						335		
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Lys	Ala	Asp	Val	Tyr	Val	Ala	Ala	Cys	Asp	Val	Pro	Gly	Ile	Lys	Arg	
		340						345					350			
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Leu	Ile	Pro	Ser	Glu	Trp	Arg	Glu	Trp	Asp	Leu	Phe	Asp	Asn	Ile	Tyr	
	355					360						365				
aaa	cta	gtt	gga	gtt	cca	gtt	gtc	act	gtt	cag	ctt	agg	tac	aat	ggg	1152
Lys	Leu	Val	Gly	Val	Pro	Val	Val	Thr	Val	Gln	Leu	Arg	Tyr	Asn	Gly	
	370					375					380					
tgg	gtg	aca	gag	atg	caa	gat	ctg	gaa	aaa	tca	agg	cag	ttg	aga	gct	1200
Trp	Val	Thr	Glu	Met	Gln	Asp	Leu	Glu	Lys	Ser	Arg	Gln	Leu	Arg	Ala	
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gca	gta	gga	ttg	gat	aat	ctt	ctt	tat	act	cca	gat	gca	gac	ttt	tct	1248
Ala	Val	Gly	Leu	Asp	Asn	Leu	Leu	Tyr	Thr	Pro	Asp	Ala	Asp	Phe	Ser	
			405					410						415		
tgt	ttt	tct	gat	ctt	gca	ctc	tcg	tcg	cct	gaa	gat	tat	tat	att	gaa	1296
Cys	Phe	Ser	Asp	Leu	Ala	Leu	Ser	Ser	Pro	Glu	Asp	Tyr	Tyr	Ile	Glu	
			420					425					430			
gga	caa	ggg	tcc	cta	ata	cag	gct	gtt	ctc	acg	cca	ggg	gat	cca	tac	1344
Gly	Gln	Gly	Ser	Leu	Ile	Gln	Ala	Val	Leu	Thr	Pro	Gly	Asp	Pro	Tyr	
	435					440						445				
atg	ccc	cta	cct	aat	gat	gca	att	ata	gaa	aga	gtt	cgg	aaa	cag	gtt	1392
Met	Pro	Leu	Pro	Asn	Asp	Ala	Ile	Ile	Glu	Arg	Val	Arg	Lys	Gln	Val	
	450					455					460					
ttg	gat	tta	ttc	cca	tcc	tct	caa	ggc	ctg	gaa	gtt	cta	tgg	tct	tcg	1440
Leu	Asp	Leu	Phe	Pro	Ser	Ser	Gln	Gly	Leu	Glu	Val	Leu	Trp	Ser	Ser	
465					470					475					480	
gtg	gtt	aaa	atc	gga	caa	tcc	cta	tat	cgg	gag	ggg	cct	gga	aag	gac	1488
Val	Val	Lys	Ile	Gly	Gln	Ser	Leu	Tyr	Arg	Glu	Gly	Pro	Gly	Lys	Asp	
				485					490					495		
cca	ttc	aga	cct	gat	cag	aag	aca	cca	gta	aaa	aat	ttc	ttc	ctt	gca	1536
Pro	Phe	Arg	Pro	Asp	Gln	Lys	Thr	Pro	Val	Lys	Asn	Phe	Phe	Leu	Ala	
			500					505						510		
ggg	tca	tac	acc	aaa	cag	gat	tac	att	gac	agt	atg	gaa	gga	gcg	acc	1584

Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr
 515 520 525
 cta tcg ggg aga caa gca gct gca tat atc tgc agc gcc ggt gaa gat 1632
 Leu Ser Gly Arg Gln Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540
 ctg gca gca ctt cgc aag aag atc gct gct gat cat cca gag caa ctg 1680
 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560
 atc aac aaa gat tct aac gtg tcg gat gaa ctg agt ctc gta taa 1725
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<210> 132

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 20 25 30
 Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala
 35 40 45
 Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys
 50 55 60
 Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala
 65 70 75 80
 Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg
 85 90 95
 Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn
 100 105 110
 His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu
 115 120 125
 Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys

130

135

140

Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu
 145 150 155 160

Asp Phe Arg Leu Pro Met Gly Ala Pro Leu His Gly Ile Arg Ala Phe
 165 170 175

Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val
 180 185 190

Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly
 195 200 205

Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp
 210 215 220

Phe Leu Ser Lys Gly Gly Thr Arg Met Ser Ile Gln Arg Met Trp Asp
 225 230 235 240

Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala
 245 250 255

Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala
 260 265 270

Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly
 275 280 285

Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg
 290 295 300

Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr
 305 310 315 320

Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val
 325 330 335

Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg
 340 345 350

Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr
 355 360 365

Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly

370

375

380

Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala
 385 390 395 400

Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser
 405 410 415

Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu
 420 425 430

Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr
 435 440 445

Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val
 450 455 460

Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser
 465 470 475 480

Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp
 485 490 495

Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala
 500 505 510

Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr
 515 520 525

Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560

Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val
 565 570

<210> 133

<211> 1848

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<400> 133

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tgc aag act gta gct ttg ggt gat agc aaa cca aga tac aat aaa cag	96
Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln	
20 25 30	
aga agt tct tgt ttt gac cct ttg ata att gga aat tgt act gat cag	144
Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln	
35 40 45	
cag cag ctt tgt ggc ttg agt tgg ggg gtg gac aag gct aag gga aga	192
Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg	
50 55 60	
aga ggg ggt act gtt tcc aat ttg aaa gca gtt gta gat gta gac aaa	240
Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys	
65 70 75 80	
aga gtg gag agc tat ggc agt agt gat gta gaa gga aat gag agt ggc	288
Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly	
85 90 95	
agc tat gat gcc att gtt ata ggt tca gga ata ggt gga ttg gtg gca	336
Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala	
100 105 110	
gcg acg cag ctg gcg gtt aag gga gct aag gtt tta gtt ctg gag aag	384
Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys	
115 120 125	
tat gtt att cct ggt gga agc tct ggc ttt tac gag agg gat ggt tat	432
Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr	
130 135 140	
aag ttt gat gtt ggt tca tca gtg atg ttt gga ttc agt gat aag gga	480
Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly	
145 150 155 160	
aac ctc aat tta att act caa gca ttg gca gca gta gga cgt aaa tta	528
Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu	
165 170 175	
gaa gtt ata cct gac cca aca act gta cat ttc cac ctg cca aat gac	576
Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp	
180 185 190	
ctt tct gtt cgt ata cac cga gag tat gat gac ttc att gaa gag ctt	624
Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu	
195 200 205	
gtg agt aaa ttt cca cat gaa aag gaa ggg att atc aaa ttt tac agt	672
Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser	
210 215 220	

gaa tgc tgg aag atc ttt aat tct ctg aat tca ttg gaa ctg aag tct Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser 225 230 235 240	720
ttg gag gaa ccc atc tac ctt ttt ggc cag ttc ttt aag aag ccc ctt Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu 245 250 255	768
gaa tgc ttg act ctt gcc tac tat ttg ccc cag aat gct ggt agc atc Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile 260 265 270	816
gct cgg aag tat ata aga gat cct ggg ttg ctg tct ttt ata gat gca Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala 275 280 285	864
gag tgc ttt atc gtg agt aca gtt aat gca tta caa aca cca atg atc Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile 290 295 300	912
aat gca agc atg gtt cta tgt gac aga cat ttt ggc gga atc aac tac Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr 305 310 315 320	960
ccc gtt ggt gga gtt ggc gag atc gcc aaa tcc tta gca aaa ggc ttg Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu 325 330 335	1008
gat gat cac gga agt cag ata ctt tat agg gca aat gtt aca agt atc Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile 340 345 350	1056
att ttg gac aat ggc aaa gct gtg gga gtg aag ctt tct gac ggg agg Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg 355 360 365	1104
aag ttt tat gct aaa acc ata gta tgc aat gct acc aga tgg gat act Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr 370 375 380	1152
ttt gga aag ctt tta aaa gct gag aat ctg cca aaa gaa gaa gaa aat Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn 385 390 395 400	1200
ttc cag aaa gct tat gta aaa gca cct tct ttt ctt tct att cat atg Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met 405 410 415	1248
gga gtt aaa gca gat gta ctc cca cca gac aca gat tgt cac cat ttt Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe 420 425 430	1296
gtc ctc gag gat gat tgg aca aat ttg gag aaa cca tat gga agt ata Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile 435 440 445	1344
ttc ttg agt att cca aca gtt ctt gat tcc tca ttg gcc cca gaa gga Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly 450 455 460	1392

cac cat att ctt cac att ttt aca aca tcg agc att gaa gat tgg gag 1440
 His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu
 465 470 475 480

gga ctc tct ccg aaa gac tat gaa gcg aag aaa gag gtt gtt gct gaa 1488
Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu
485 490 495

agg att ata agc aga ctt gaa aaa aca ctc ttc cca ggg ctt aag tca 1536
Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser
500 505 510

tct att ctc ttt aag gag gtg gga act cca aag acc cac aga cga tac 1584
Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr
515 520 525

ctt gct cgt gat agt ggt acc tat gga cca atg cca cgc gga aca cct 1632
Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro
530 535 540

aag gga ctc ctg gga atg cct ttc aat acc act gct ata gat ggt cta 1680
Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu
545 550 555 560

tat	tgt	gtt	ggc	gat	agt	tgc	ttc	cca	gga	caa	ggg	gtt	ata	gct	gta	1728
Tyr	Cys	Val	Gly	Asp	Ser	Cys	Phe	Pro	Gly	Gln	Gly	Val	Ile	Ala	Val	
				565					570					575		

gcc ttt tca gga gta atg tgc gct cat cgt gtt gca gct gac tta ggg 1776
Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly
580 585 590

ttt gaa aaa aaa tca gat gtg ctg gac agt gct ctt ctt aga cta ctt 1824
Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu
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ggt tgg tta agg aca cta gca tga 1848
Gly Trp Leu Arg Thr Leu Ala
610 615

<210> 134

<211> 615

<212> PRT

<213> Lycopersicon esculentum

<400> 134

Met Cys Thr Leu Ser Phe Met Tyr Pro Asn Ser Leu Leu Asp Gly Thr
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Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln
20 25 30

Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln

35	40	45																	
Gln	Gln	Leu	Cys	Gly	Leu	Ser	Trp	Gly	Val	Asp	Lys	Ala	Lys	Gly	Arg				
50						55					60								
Arg	Gly	Gly	Thr	Val	Ser	Asn	Leu	Lys	Ala	Val	Val	Asp	Val	Asp	Lys				
65					70					75					80				
Arg	Val	Glu	Ser	Tyr	Gly	Ser	Ser	Asp	Val	Glu	Gly	Asn	Glu	Ser	Gly				
				85					90					95					
Ser	Tyr	Asp	Ala	Ile	Val	Ile	Gly	Ser	Gly	Ile	Gly	Gly	Leu	Val	Ala				
			100					105					110						
Ala	Thr	Gln	Leu	Ala	Val	Lys	Gly	Ala	Lys	Val	Leu	Val	Leu	Glu	Lys				
		115					120					125							
Tyr	Val	Ile	Pro	Gly	Gly	Ser	Ser	Gly	Phe	Tyr	Glu	Arg	Asp	Gly	Tyr				
	130					135					140								
Lys	Phe	Asp	Val	Gly	Ser	Ser	Val	Met	Phe	Gly	Phe	Ser	Asp	Lys	Gly				
145					150					155					160				
Asn	Leu	Asn	Leu	Ile	Thr	Gln	Ala	Leu	Ala	Ala	Val	Gly	Arg	Lys	Leu				
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Glu	Val	Ile	Pro	Asp	Pro	Thr	Thr	Val	His	Phe	His	Leu	Pro	Asn	Asp				
			180					185					190						
Leu	Ser	Val	Arg	Ile	His	Arg	Glu	Tyr	Asp	Asp	Phe	Ile	Glu	Glu	Leu				
		195					200					205							
Val	Ser	Lys	Phe	Pro	His	Glu	Lys	Glu	Gly	Ile	Ile	Lys	Phe	Tyr	Ser				
		210				215					220								
Glu	Cys	Trp	Lys	Ile	Phe	Asn	Ser	Leu	Asn	Ser	Leu	Glu	Leu	Lys	Ser				
225					230					235					240				
Leu	Glu	Glu	Pro	Ile	Tyr	Leu	Phe	Gly	Gln	Phe	Phe	Lys	Lys	Pro	Leu				
				245					250					255					
Glu	Cys	Leu	Thr	Leu	Ala	Tyr	Tyr	Leu	Pro	Gln	Asn	Ala	Gly	Ser	Ile				
			260					265					270						
Ala	Arg	Lys	Tyr	Ile	Arg	Asp	Pro	Gly	Leu	Leu	Ser	Phe	Ile	Asp	Ala				

275

280

285

Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile
 290 295 300

Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr
 305 310 315 320

Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu
 325 330 335

Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile
 340 345 350

Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg
 355 360 365

Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr
 370 375 380

Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn
 385 390 395 400

Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met
 405 410 415

Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe
 420 425 430

Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile
 435 440 445

Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly
 450 455 460

His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu
 465 470 475 480

Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu
 485 490 495

Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser
 500 505 510

Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr

515

520

525

Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro
 530 535 540

Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu
 545 550 555 560

Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val
 565 570 575

Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly
 580 585 590

Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu
 595 600 605

Gly Trp Leu Arg Thr Leu Ala
 610 615

<210> 135

<211> 1233

<212> DNA

<213> Tagetes erecta

<220>

<221> CDS

<400> 135

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tct tct tca atc tct act ggc tgt tca ctc tcc ccc ttc ttc ctc aaa 96
 Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys
 20 25 30

tca tct tct cat tcc cct aac cct cgc cga cac cgc cgc tcc gcc gta 144
 Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val
 35 40 45

tgc tgc tct ttc gcc tca ctc gac tct gca aaa atc aaa gtc gtt ggc 192
 Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly
 50 55 60

gtc ggt ggt ggt ggc aac aat gcc gtt aac cgc atg att ggt agc ggc 240
 Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly
 65 70 75 80

tta cag ggt gtt gat ttt tac gcc att aac acg gac tca caa gcg ctt	288
Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu	
85 90 95	
ctg caa tct gtt gca cat aac cct att caa att ggg gag ctt ttg act	336
Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr	
100 105 110	
cgt gga tta ggt act ggt ggg aac ccg ctt ttg gga gaa cag gct gcg	384
Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala	
115 120 125	
gag gag tcg aag gaa gcg att ggg aat gcg ctt aaa ggg tcg gat ctt	432
Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu	
130 135 140	
gtg ttt ata aca gca ggt atg ggt ggt ggg acg ggt tcg ggt gct gct	480
Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala	
145 150 155 160	
cca gtt gta gcg cag ata gcg aaa gaa gca ggg tat tta act gtt ggt	528
Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly	
165 170 175	
gtt gta acg tac cca ttc agc ttt gaa ggc cgt aaa aga tca gta cag	576
Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln	
180 185 190	
gcg tta gag gct att gag aag ctg caa aag aac gtt gac aca ctt ata	624
Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile	
195 200 205	
gtg att cca aat gac cgt ttg ctg gat att gct gat gaa aac acg cct	672
Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro	
210 215 220	
ctt cag gat gct ttt ctt ctt gct gat gat gta ctc cgc caa gga gtt	720
Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val	
225 230 235 240	
caa gga atc tca gat ata att aca ata cct ggg ctg gta aat gtg gac	768
Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp	
245 250 255	
ttt gca gac gtt aaa gca gtc atg aaa gat tct gga act gca atg ctt	816
Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu	
260 265 270	
ggg gtc ggt gtt tcc tca agt aaa aac cga gct gaa gaa gca gct gaa	864
Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu	
275 280 285	
caa gca act ctt gct cct ttg att gga tca tca att caa tct gct aca	912
Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr	
290 295 300	
ggg gtt gtt tat aat att acc gga ggg aag gac ata act cta caa gaa	960
Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu	
305 310 315 320	

gtc aac agg gtt tct cag gtg gta aca agt ttg gca gat cca tca gca 1008
 Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala
 325 330 335

aac att ata ttc ggg gca gtg gta gat gag aga tac aac ggg gag att 1056
 Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile
 340 345 350

cat gtg acc att gtt gct act ggc ttt gcc cag tcg ttt cag aaa tct 1104
 His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser
 355 360 365

ctt ctt gct gac ccg aaa gga gca aaa ctt gtt gat aga aat caa gaa 1152
 Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

cct aca caa cct ttg act tcc gcg aga tct ttg aca aca cct tct cct 1200
 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

gct ccg tct cgg tct agg aaa ctc ttc ttt taa 1233
 Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
 405 410

<210> 136

<211> 410

<212> PRT

<213> Tagetes erecta

<400> 136

Met Ala Thr His Lys Leu Leu Gln Phe Thr Thr Asn Leu Pro Pro Ser
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Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys
 20 25 30

Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val
 35 40 45

Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly
 50 55 60

Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly
 65 70 75 80

Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu
 85 90 95

Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr

100

105

110

Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala
 115 120 125

Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu
 130 135 140

Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala
 145 150 155 160

Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly
 165 170 175

Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln
 180 185 190

Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile
 195 200 205

Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro
 210 215 220

Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val
 225 230 235 240

Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp
 245 250 255

Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu
 260 265 270

Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu
 275 280 285

Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr
 290 295 300

Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu
 305 310 315 320

Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala
 325 330 335

Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile

340

345

350

His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser
 355 360 365

Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
 405 410

<210> 137

<211> 891

<212> DNA

<213> Tagetes erecta

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<221> CDS

<400> 137

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act	ttc	ccc	aca	ttc	aat	ccc	cta	cac	aaa	acc	cta	act	aaa	cca	aca	96
Thr	Phe	Pro	Thr	Phe	Asn	Pro	Leu	His	Lys	Thr	Leu	Thr	Lys	Pro	Thr	
			20					25					30			
cca	aaa	ccc	tac	cca	aag	cca	cca	cca	att	cgc	tcc	gtc	ctt	caa	tac	144
Pro	Lys	Pro	Tyr	Pro	Lys	Pro	Pro	Pro	Ile	Arg	Ser	Val	Leu	Gln	Tyr	
			35					40					45			
aat	cgc	aaa	cca	gag	ctc	gcc	gga	gac	act	cca	cga	gtc	gtc	gca	atc	192
Asn	Arg	Lys	Pro	Glu	Leu	Ala	Gly	Asp	Thr	Pro	Arg	Val	Val	Ala	Ile	
			50				55				60					
gac	gcc	gac	gtt	ggt	cta	cgt	aac	ctc	gat	ctt	ctt	ctc	ggt	ctc	gaa	240
Asp	Ala	Asp	Val	Gly	Leu	Arg	Asn	Leu	Asp	Leu	Leu	Leu	Gly	Leu	Glu	
65				70				75						80		
aac	cgc	gtc	aat	tac	acc	gtc	gtt	gaa	gtt	ctc	aac	ggc	gat	tgc	aga	288
Asn	Arg	Val	Asn	Tyr	Thr	Val	Val	Glu	Val	Leu	Asn	Gly	Asp	Cys	Arg	
			85					90					95			
ctc	gac	caa	gcc	cta	gtt	cgt	gat	aaa	cgc	tgg	tca	aat	ttc	gaa	ttg	336
Leu	Asp	Gln	Ala	Leu	Val	Arg	Asp	Lys	Arg	Trp	Ser	Asn	Phe	Glu	Leu	
			100					105					110			

ctt tgt att tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly 115 120 125	384
aaa gct tta gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys 130 135 140	432
ccg gat ttt ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe 145 150 155 160	480
ata acc gcc att aca ccg gct aac gaa gcc gta tta gtt aca aca cct Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro 165 170 175	528
gat att act gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu 180 185 190	576
tgt gat gga att agg gat att aaa atg att gtg aac aga gtt aga act Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr 195 200 205	624
gat ttg ata agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu 210 215 220	672
atg ttg gga ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile 225 230 235 240	720
cgg agt acg aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr 245 250 255	768
tta gca gga ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln 260 265 270	816
gat agc atg aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly 275 280 285	864
ttt ttc tcg ttt ttt gga ggt tag tga Phe Phe Ser Phe Phe Gly Gly 290 295	891

<210> 138

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<212> PRT

<213> Tagetes erecta

<400> 138

Met	Thr	Ser	Leu	Arg	Phe	Leu	Thr	Glu	Pro	Ser	Leu	Val	Cys	Ser	Ser	1	5	10	15
Thr	Phe	Pro	Thr	Phe	Asn	Pro	Leu	His	Lys	Thr	Leu	Thr	Lys	Pro	Thr	20	25	30	
Pro	Lys	Pro	Tyr	Pro	Lys	Pro	Pro	Pro	Ile	Arg	Ser	Val	Leu	Gln	Tyr	35	40	45	
Asn	Arg	Lys	Pro	Glu	Leu	Ala	Gly	Asp	Thr	Pro	Arg	Val	Val	Ala	Ile	50	55	60	
Asp	Ala	Asp	Val	Gly	Leu	Arg	Asn	Leu	Asp	Leu	Leu	Leu	Gly	Leu	Glu	65	70	75	80
Asn	Arg	Val	Asn	Tyr	Thr	Val	Val	Glu	Val	Leu	Asn	Gly	Asp	Cys	Arg	85	90	95	
Leu	Asp	Gln	Ala	Leu	Val	Arg	Asp	Lys	Arg	Trp	Ser	Asn	Phe	Glu	Leu	100	105	110	
Leu	Cys	Ile	Ser	Lys	Pro	Arg	Ser	Lys	Leu	Pro	Leu	Gly	Phe	Gly	Gly	115	120	125	
Lys	Ala	Leu	Val	Trp	Leu	Asp	Ala	Leu	Lys	Asp	Arg	Gln	Glu	Gly	Cys	130	135	140	
Pro	Asp	Phe	Ile	Leu	Ile	Asp	Cys	Pro	Ala	Gly	Ile	Asp	Ala	Gly	Phe	145	150	155	160
Ile	Thr	Ala	Ile	Thr	Pro	Ala	Asn	Glu	Ala	Val	Leu	Val	Thr	Thr	Pro	165	170	175	
Asp	Ile	Thr	Ala	Leu	Arg	Asp	Ala	Asp	Arg	Val	Thr	Gly	Leu	Leu	Glu	180	185	190	
Cys	Asp	Gly	Ile	Arg	Asp	Ile	Lys	Met	Ile	Val	Asn	Arg	Val	Arg	Thr	195	200	205	
Asp	Leu	Ile	Arg	Gly	Glu	Asp	Met	Met	Ser	Val	Leu	Asp	Val	Gln	Glu	210	215	220	
Met	Leu	Gly	Leu	Ser	Leu	Leu	Ser	Asp	Thr	Arg	Gly	Phe	Glu	Val	Ile	225	230	235	240

Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
 245 250 255

Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
 260 265 270

Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly
 275 280 285

Phe Phe Ser Phe Phe Gly Gly
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<210> 139

<211> 332

<212> DNA

<213> Tagetes erecta

<220>

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<400> 139

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Lys	Leu	Ala	Arg	Ala	Ser	Leu	Tyr	Phe	Tyr	Thr	Ser	Met	Ala	Ala	Ala	
1				5					10				15			

att	gct	gtc	cct	tgt	agc	tca	aga	cca	ttt	ggc	tta	ggg	cga	atg	cgg	96
Ile	Ala	Val	Pro	Cys	Ser	Ser	Arg	Pro	Phe	Gly	Leu	Gly	Arg	Met	Arg	
			20					25					30			

tta	ctt	ggg	cat	aaa	ccc	aca	acc	ata	act	tgt	cac	ttc	ccc	ttt	tct	144
Leu	Leu	Gly	His	Lys	Pro	Thr	Thr	Ile	Thr	Cys	His	Phe	Pro	Phe	Ser	
		35					40				45					

ttt	tct	atc	aaa	tca	ttt	acc	cca	att	gtt	agg	ggc	aga	aga	tgt	act	192
Phe	Ser	Ile	Lys	Ser	Phe	Thr	Pro	Ile	Val	Arg	Gly	Arg	Arg	Cys	Thr	
		50				55					60					

gtt	tgt	ttt	gtt	gcc	ggg	ggc	gac	agt	aat	agt	aac	agt	aat	aat	aat	240
Val	Cys	Phe	Val	Ala	Gly	Gly	Asp	Ser	Asn	Ser	Asn	Ser	Asn	Asn	Asn	
65				70					75					80		

agt	gac	agt	aat	agt	aat	aat	ccg	ggg	ctg	gat	tta	aac	ccg	gcg	gtt	288
Ser	Asp	Ser	Asn	Ser	Asn	Asn	Pro	Gly	Leu	Asp	Leu	Asn	Pro	Ala	Val	
			85						90					95		

atg	aac	cgt	aac	cgt	ttg	gtt	gaa	gaa	aaa	atg	gag	agg	tcg	ac		332
Met	Asn	Arg	Asn	Arg	Leu	Val	Glu	Glu	Lys	Met	Glu	Arg	Ser			
			100					105					110			

<210> 140

<211> 110

<212> PRT

<213> Tagetes erecta

<400> 140

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Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
 85 90 95

Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

<210> 141

<211> 332

<212> DNA

<213> Tagetes erceta

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<221> misc_feature

<223> beta-Hydroxylase Sense Fragment

<400> 141

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tgtagctcaa gaccatttgg cttagggtcga atgcgggttac ttgggtcataa acccacaacc 120

ataacttgtc acttcccctt ttctttttct atcaaatcat ttaccccaat tgttaggggc 180

agaagatgta ctgtttgttt tgttgccggt ggcgacagta atagtaacag taataataat 240
 agtgacagta atagtaataa tccgggtctg gatttaaacc cggcgggttat gaaccgtaac 300
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<211> 332

<212> DNA

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<223> beta-Hydroxylase Antisense Fragment

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 ttgtagctca agaccatttg gcttaggtcg aatgcggtta cttggtcata aaccacaa 120
 cataacttgt cacttccctt tttctttttc tatcaaatca tttaccccaa ttgttagggg 180
 cagaagatgt actgtttggt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240
 tagtgacagt aatagtaata atccgggtct ggatttaaacc cggcgggtta tgaaccgtaa 300
 ccgtttggtt gaagaaaaaa tggagaggat cc 332